

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:08:56 ; Search time 46' Seconds
(without alignments)
1169.243 Million cell updates/sec

Title: US-10-633-835-2

Perfect score: 2907

Sequence: 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPPADLAV 559

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2896	99.6	2185	1 S60200	acetyl-CoA carboxy
2	2190	75.3	2288	2 T30568	acetyl-CoA carboxy
3	2090.5	71.9	2280	2 T38906	acetyl-CoA carboxy
4	2060	70.9	2233	2 S63347	acetyl-CoA carboxy
5	2060	70.9	2279	2 T42531	acetyl-CoA carboxy
6	1785	61.4	2345	1 A35578	acetyl-CoA carboxy
7	1782	61.3	2339	2 S41121	acetyl-CoA carboxy
8	1781	61.3	2346	2 T38928	acetyl-CoA carboxy
9	1780	61.2	2324	1 A29924	acetyl-CoA carboxy
10	1754.5	60.4	2123	2 S55089	probable acetyl-Co
11	1598.5	55.0	640	2 T07923	acetyl-CoA carboxy
12	1583	54.5	2304	2 T07920	probable acetyl-Co
13	1581.5	54.4	2359	2 E86483	probable acetyl-Co
14	1579	54.3	2257	2 D86483	protein F505.19 [i
15	1577.5	54.3	2257	2 T09538	acetyl-CoA carboxy
16	1569.5	54.0	2311	2 T06161	acetyl-CoA carboxy
17	1565	53.8	2257	1 A57710	acetyl-CoA carboxy
18	1558.5	53.6	2261	2 T07084	acetyl-CoA carboxy
19	1555.5	53.5	1978	2 T07081	acetyl-CoA carboxy
20	1543.5	53.1	2325	2 T02235	acetyl-CoA carboxy
21	1502.5	51.7	2089	1 A48757	acetyl-CoA carboxy
22	1314	45.2	2054	2 T32413	probable acetyl-Co
23	1121	38.6	1657	2 T25421	hypothetical prote
24	769	26.5	371	2 T07938	probable acetyl-Co
25	724	24.9	491	2 A69123	biotin carboxylase
26	709.5	24.4	447	2 AH1923	biotin carboxylase
27	709.5	24.4	447	2 A53311	biotin carboxylase
28	679	23.4	453	2 H81978	probable acetyl-Co
29	676	23.3	450	2 A69581	acetyl-CoA carboxy

RESULT 1

S60200

acetyl-CoA carboxylase (EC 6.4.1.2) - smut fungus (Ustilago maydis)

C:Species: Ustilago maydis (corn smut)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S60200; S49391

R:Bailey, A.; Keon, J.; Owen, J.; Hargreaves, J.

Mol. Gen. Genet. 249, 191-201, 1995

A:Title: The ACC1 gene, encoding acetyl-CoA carboxylase, is essential for growth in Ustilago maydis

A:Reference number: S60200; MUID:96086936; PMID:7500941

A:Accession: S60200

A:Molecule type: DNA

A:Residues: 1-2185 <BAI>

A:Cross-references: UNIPROT:Q12721; UNIPARC:UPI000006A8BA; EMBL:Z46886; NID:g600097; P:

C:Genetics:

A:Gene: ACC1

A:Introns: 14/1

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin

C:Keywords: biotin binding; ligase

F:41-548/Domain: biotin carboxylase homology <BCH>

F:675-747/Domain: lipoyl/biotin-binding homology <LPB>

F:714/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 99.6%; Score 2896; DB 1; Length 2185;

Best Local Similarity 99.6%; Pred. No. 1.9e-197;

Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFTIRKQGGHSVITKVLICNNGIAAVKEIRSKW 60

DB 2 PPPDHKAVSQFIGGNPLETAPASPVADFTIRKQGGHSVITKVLICNNGIAAVKEIRSKW 61

QY 61 AYETFGDERAIEFTVMTAPEDLKNVADYRMADQYVEVPGGNNNNYANVDLIVDAERA 120

DB 62 AYETFGDERAIEFTVMTAPEDLKNVADYRMADQYVEVPGGNNNNYANVDLIVDAERA 121

QY 121 GVHAWAGWGHASENPRIPESLAASKHKIIIFPGPGSAMRSLGDKLISSTIVAQHADVPCM 180

DB 122 GVHAWAGWGHASENPRIPESLAASKHKIIIFPGPGSAMRSLGDKLISSTIVAQHADVPCM 181

QY 181 PWSGTGIIKETWMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASGGGGKGI 240

DB 182 PWSGTGIIKETWMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASGGGGKGI 241

QY 241 RKCTNGEEFVKOLYNALVGEVPGSPVFMKLAQAQARHLEVQLLADQYGNASIFGRDCSVQ 300

DB 242 RKCTNGEEFVKOLYNALVGEVPGSPVFMKLAQAQARHLEVQLLADQYGNASIFGRDCSVQ 301

QY 301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVAGTVEWLYSPESGFALFLNLP 360

DB 302 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVAGTVEWLYSPESGFALFLNLP 361

QY 361 RLQVEHPITTEVMGYNIPAAQLQVAMGIPLYSIRDIRTYLGYMDPRGNEVIDDFSSPESF 420

ALIGNMENTS

30	675	23.2	506	2	D69277	biotin carboxylase
31	671.5	23.1	448	2	S74380	biotin carboxylase
32	668	23.0	455	2	G71860	biotin carboxylase
33	667	22.9	453	2	F81033	acetyl-CoA carboxy
34	666	22.9	662	2	G95929	probable methylcro
35	662	22.8	458	2	B64566	biotin carboxylase
36	660.5	22.7	667	2	AB3352	propionyl-CoA carb
37	660	22.7	452	2	C83998	acetyl-CoA carboxy
38	658.5	22.7	445	2	B75558	acetyl-CoA carboxy
39	656.5	22.6	667	2	F98286	hypothetical prote
40	656.5	22.6	677	2	AC2997	hypothetical prote
41	655.5	22.5	455	2	B86722	biotin carboxylase
42	653.5	22.5	448	2	G87482	acetyl-CoA carboxy
43	649	22.3	501	2	D64453	biotin carboxylase
44	645	22.2	449	1	J50632	acetyl-CoA carboxy
45	642	22.1	449	2	H91144	hypothetical prote

Db 362 RLQVEHPTTEMSGVNIIPAQLQVANGIPLYSIRDIRTYLGYMDPRGNEVIDDFSPSPSF 421
QY 421 KTQRKPPQGHVACRITAENPDTPGKPGMGALTELNFSSSTSTWGYFSGTSGALHEYA 480
Db 422 KTQRKPPQGHVACRITAENPDTPGKPGMGALTELNFSSSTSTWGYFSGTSGALHEYA 481
QY 481 DSQFGHIFAYGADRSEARKOMVLSKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 540
Db 482 DSQFGHIFAYGADRSEARKOMVLSKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 541
QY 541 DGLIQDLRTAERPPADLAV 559
Db 542 DGLIQDLRTAERPPADLAV 560
RESULT 2
T30568
acetyl-CoA carboxylase (EC 6.4.1.2) - Emericella nidulans
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30568
R:Morris, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A:Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergillus
A:Reference number: Z20869; MUID:99087906; PMID:9871120
A:Accession: T30568
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2288 <MOR>
A:Cross-references: UNIPROT:O60033; UNIPARC:UPI00006C49E; EMBL:Y15996; NID:G3021302; PI
C:Genetics:
A:Gene: accA
A:Introns: 54/3; 111/3
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C:Keywords: ligase

Query Match 75.3%; Score 2190; DB 2; Length 2288;
Best Local Similarity 74.8%; Pred. No. 3.8e-147;
Matches 415; Conservative 53; Mismatches 87; Indels 0; Gaps 0;
QY 5 HKAVSQFIGGNPLETAPASPVADFTIRKQGGHVSITKVLICNNGLIAAVKEIRSKWAYET 64
Db 19 HNLPSHFIGNHLDAAAPSVKDFVANHGHVSITSLIANNGLIAAVKEIRSKWAYET 78
QY 65 FGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDVAERAGVHA 124
Db 79 FGNRAIQFTVMATPEDLAANADYIRMDQYVEVPGSGNNNNYANVDLIVDVAERMDVHA 138
QY 125 VWAGCHASENPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSG 184
Db 139 VWAGCHASENPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSG 198
QY 185 TGIKETMDSQDGLTVSDVYQQACIHTAEGLKAEKIGYPMVKASGGGKGIRKCT 244
Db 199 TGVDEVKVDGVLTVVEEVYNGKCTFSPGEGLEKAKIQFGPMVKASGGGKGIRKVE 258
QY 245 NGEFFKQLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNATISIFGRDCSVORRHQ 304
Db 259 KEEDFINLYNAANEIPGSPIFIMKLAGNARHLEVQLLADQYGNATISIFGRDCSVORRHQ 318
QY 305 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNPRLQV 364
Db 319 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGYVSAGTVEWLYSHADDKYFLELNPRLQV 378
QY 365 EHPTEWMSGVNIIPAQLQVANGIPLYSIRDIRTYLGYMDPRGNEVIDDFSPSPSF 424
Db 379 EHPTEWMSGVNIIPAQLQVANGIPLYSIRDIRTYLGYMDPRGNEVIDDFSPSPSF 438
QY 425 KPQCGHVACRITAENPDTPGKPGMGALTELNFSSSTSTWGYFSGTSGALHEYADSO 484
Db 439 RQPKGHTTACRTSDPDGEGFKPSSGTWHELNFRSSNVWGYFSGTAGGTHSPSDSO 498

QY 485 GHIFAYGADRSEARKOMVLSKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 544
Db 499 GHIFAYGADRSEARKOMVLSKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 558
QY 545 QDLRTAERPPADLAV 559
Db 559 SNKLTAEPPDTTIAV 573
RESULT 3
T38906
acetyl-CoA carboxylase (EC 6.4.1.2) [similarity] - fission yeast (Schizosaccharomyces f
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38906
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21813
A:Accession: T38906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2280 <CON>
A:Cross-references: UNIPROT:P78820; UNIPARC:UPI0000127CAE; EMBL:Z99261; PIDN:CAB16395.1
A:Experimental source: strain 972h-; cosmid c5624
C:Genetics:
A:Gene: SPDB:SPAC56E4.04C
A:Map position: 1
A:Introns: 44/1
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C:Keywords: ligase
Query Match 71.9%; Score 2090.5; DB 2; Length 2280;
Best Local Similarity 71.4%; Pred. No. 4.6e-140;
Matches 396; Conservative 62; Mismatches 96; Indels 1; Gaps 1;
QY 6 KAVSQFIGGNPLETAPASPVADFTIRKQGGHVSITKVLICNNGLIAAVKEIRSKWAYET 65
Db 37 RVASHFPGNSLDKAPACKVXDYASHGHVITSLIANNGLIAAVKEIRSKWAYET 96
QY 66 GDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDVAERAGVHA 125
Db 97 NNERAIKFTVMATPDDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDVAERAGVHA 156
QY 126 WAGCHASENPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSG 185
Db 157 WAGCHASENPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSG 216
QY 186 GIKETMDSQDGLTVSDVYQQACIHTAEGLKAEKIGYPMVKASGGGKGIRKCT 244
Db 217 ELDQVRIDEETNIVTVDDVYQKACIRSAEGIAVAEKIGYPMVKASGGGKGIRQVT 276
QY 245 NGEFFKQLYNAVLEVPSPVFMKLAGQARHLEVQLLADQYGNATISIFGRDCSVORRHQ 304
Db 277 STEKFAQAFQVLDLPSPVFMKLAGQARHLEVQLLADQYGNATISIFGRDCSVORRHQ 336
QY 305 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNPRLQV 364
Db 337 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNPRLQV 396
QY 365 EHPTEWMSGVNIIPAQLQVANGIPLYSIRDIRTYLGYMDPRGNEVIDDFSPSPSF 424
Db 397 EHPTEWMSGVNIIPAQLQVANGIPLYSIRDIRTYLGYMDPRGNEVIDDFSPSPSF 456
QY 425 KPQCGHVACRITAENPDTPGKPGMGALTELNFSSSTSTWGYFSGTSGALHEYADSO 484
Db 457 VPTPKGHCACRTSDPDGEGFKPSSGTWHELNFRSSNVWGYFSGTAGGTHSPSDSO 516
QY 485 GHIFAYGADRSEARKOMVLSKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 544
Db 517 GHIFABRESRSRKMVVALKELSIKELSGDFTTVEYLKLETDAPESNKITGWL 576
QY 545 QDLRTAERPPADLAV 559

Db 577 AQVTSARPDKLAV 591
RESULT 4
S63347
acetyl-CoA carboxylase (EC 6.4.1.2) - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein N3175; protein YNR016c
C;Species: *Saccharomyces cerevisiae*
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63347; S31249
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63347
A;Molecule type: DNA
A;Residues: 1-2233 <POH>
A;Cross-references: UNIPROT:Q00955; UNIPARC:UPI0000127CAF; EMBL:Z71631; NID:g1302497; PI
A;Experimental source: strain S288C
R;Al-Feel, W.; Chirala, S.S.; Wakil, S.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 4534-4538, 1992
A;Title: Cloning of the yeast FAS3 gene and primary structure of yeast acetyl-CoA carboxylase
A;Reference number: S31249; MUID:92262474; PMID:1350093
A;Accession: S31249
A;Molecule type: DNA
A;Residues: 1-1522, 'G', 1524-1755, 'MYRCL', 1756-1760, 'ESTN', 1761, 1767-2233 <ALF>
A;Cross-references: UNIPARC:UPI0000145F95; EMBL:M92156; NID:g402313; PIDN:AAA20073.1; PI
C;Genetics:
A;Gene: SGD:ACC1; FAS3; ABP2
A;Cross-references: SGD:S0005299; MIPS:YNR016c
A;Map position: 14R
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
F;61-569/Domain: biotin binding; fatty acid biosynthesis; ligase
F;696-768/Domain: lipoyl/biotin-binding homology <LBP>
F;735/Binding site: biotin (Lys) (covalent) #status Predicted
Query Match 70.9%; Score 2060; DB 2; Length 2233;
Best Local Similarity 69.1%; Pred. No. 6.6e-138;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;
QY 3 PDHKAVSQFTGPNLETPAPASPVADFIKQGHSHVITKVLICNNGIAAATKESIRKWAY 62
Db 29 PGH-----FGLNTVDKLESPDLDFVKSCHGHTVTSKILIANNGIAAATKESIRKWAY 83
QY 63 ETQCDERAEFTWATPEDLKNADYIRMAQDVVEVPGSGNNNNYANVDLIIVDAERAGV 122
Db 84 ETFGDDRTQVAMATPEDLEANAETIRMAQDVIEVPGGTNNNNYANVDLIIVDAERADY 143
QY 123 HAVWAGHGHASENPRLPESLAASKHKIIFIGPPGSAMRSISLGDKI SSTIVAQHADVPMPW 182
Db 144 DAVWAGHGHASENPLLPESLSQSKRKVIFIGPPGNAMRSISLGDKI SSTIVAQSAKVPICPW 203
QY 183 SGTGKETWMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPVMIKASGGGKGKI 240
Db 204 SGTGV-DTVHDEKTLGVSDVDIYQGCCTSPEDGLQAKRIGFPVMIKASGGGKGKI 262
QY 241 RKTNGEEFKQLNVLGEPVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 300
Db 263 QVERBEDFTALYHQANETIPGSPIFTMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 322
QY 301 RRHOKIIEAPVTIAPEDARESEKAAVRLAKLVGVYSAGTVEMWLYSPESGEFAFLNLP 360
Db 323 RRHOKIIEAPVTIAPEDARESEKAAVRLAKLVGVYSAGTVEMWLYSHDDGKFFYLENP 382
QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVDIDFSSPES 420
Db 383 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVDIDFSSPES 442
QY 421 KTQRKPOQGHVVACRITAENPDTPGKPGMGALTELNFRSSTSTWGVSVGTSGALHEYA 480
Db 443 KKQRRPIPKGHCTACRITSDPDNDGPKPGSGTTLHNLNFRSSNNVWGVSVGNNGNIHSPS 502
QY 481 DSQFGHIFAYGADRSEARKQMWISLSELSIRGDFRTTVEYLIKLETDAPESNKITITGWL 540

Db 503 DSQFGHIFAYGADRSEARKQMWISLSELSIRGDFRTTVEYLIKLETDAPESNKITITGWL 562
QY 541 DGLIQRLTAERPPADLAV 559
Db 563 DLLITHKMTAERKPDPTLAV 581
RESULT 5
T42531
acetyl-CoA carboxylase (EC 6.4.1.2) - fission yeast (*Schizosaccharomyces pombe*)
N;Alternate names: acetyl-coenzyme A carboxylase
C;Species: *Schizosaccharomyces pombe*
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2002
C;Accession: T42531
R;Saico, A.; Kazuta, Y.; Toh, H.; Kondo, H.; Tanabe, T.
submitted to the EMBL Data Library, October 1997
A;Description: Biotin-dependent enzymes in *Schizosaccharomyces pombe*: cloning and nucl
A;Reference number: Z22171
A;Accession: T42531
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2279 <SAI>
A;Cross-references: UNIPARC:UPI00001690FB; EMBL:D78169; PIDN:BAA11238.1
A;Experimental source: strain HM123
C;Genetics:
A;Introns: 44/1
C;Function:
A;Description: catalyzes the carboxylation of acetyl-CoA to malonyl-CoA using carboxyl
A;Pathway: fatty acid biosynthesis
A;Note: committed step of fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C;Keywords: biotin metabolism; fatty acid biosynthesis; ligase
Query Match 70.9%; Score 2060; DB 2; Length 2279;
Best Local Similarity 70.6%; Pred. No. 6.8e-138;
Matches 392; Conservative 64; Mismatches 97; Indels 2; Gaps 2;
QY 6 KAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAATKESIRKWAYEYF 65
Db 37 RVASHFLGNSLDKAPAGKVDYIASHGGHTVITSILIANNGIAAATKESIRKWAYEYF 96
QY 66 GDERAEFTWATPEDLKNADYIRMAQDVVEVPGSGNNNNYANVDLIIVDAERAGVAV 125
Db 97 NNERAIKFTWATPDLLKNADYIRMAQDVVEVPGSGNNNNYANVDLIIVDAERAGVAV 156
QY 126 WAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSISLGDKI SSTIVAQHADVPMPWSGT 185
Db 157 WAGWGHASENPKLPESLSASSKKIIFIGPPGSAMRSISLGDKI SSTIVAQSAKVPICMSWGN 216
QY 186 GIKETWMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPVMIKASGGGKGIRKCT 244
Db 217 ELDOVRIDETNIVTDDVYQACIRSAEGLIAVAEKIGYSVMIKASGGGKGIRQVT 276
QY 245 NGEERKQLNVLGEPVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVORRHQ 304
Db 277 STEKFAQAFQQVLDDELPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVORRHQ 336
QY 305 KIIEEAPVTIAPEDARESEKAAVRLAKLVGVYSAGTVEMWLYSPESGEFAFLNLP 364
Db 337 KIL-EAPVTIAPATFHEMERAAVRLGELVGVASAGTIEYLYEPENDRDFVLELNP 395
QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVDIDFSSPESFKTOR 424
Db 396 EHPTTEMVSGVNIIPAAQLQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFQNPESKVKQ 455
QY 425 KPQOPGHVVACRITAENPDTPGKPGMGALTELNFRSSTSTWGVSVGTSGALHEYADSO 484
Db 456 VFTPKGHCVACRITSDPDNDGPKPGSGTTLHNLNFRSSNNVWGVSVGTAGTHFSDSO 515
QY 485 GHIFAYGADRSEARKQMWISLSELSIRGDFRTTVEYLIKLETDAPESNKITITGWL 544
Db 516 GHIFSTESSESRKSMVVALKELSGIRGDFRTTVEYLIKLETDAPESNEFTTGWLDRLI 575

102 ASP-AEFVTRPGNKVIEKVLINAGIAVYKMSRIRWSYEMFRNERAIRFVVMVTPED 160

82 LKVNADYIRMAOQYVEVPGSGNNNNYANVDLIVDVAERAGVHVAWAGWGHASENPRLPES 141

161 LKNAEYIKMADHYVPVPGGANNNNYANVELIIDIAKRIIPVQAVWAGWGHASENPKLP 220

142 LAASKHKLIIFPGPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKIKETWMSD---QGFL 198

221 LL--KNGIAPMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLRVDQWENDFSKRIL 278

199 TVSDDDVYQQAICHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNAYLG 258

279 NVPQDIYEKGVKVDVDDLKAAEEVGPVMIKASEGGGKGIKRVNNADDPPNLFQVQA 338

259 EYVSPVFNKLAGOARHLEVLQADQYGNASIFGRDCSVQRHOKIIEBAPTIIAPED 318

339 EYVSPFIVNRLAKSRHLEVLQADQYGNASIFGRDCSVQRHOKIIEBAPAIATPA 398

319 ARSEMEKAAVRLAKLYGVYSAGTVEMLYSPESGEFALELNPRLOQVHEPTTWMYSGVNP 378

399 VFSEHQCAVKLAKMVGYSAGTVELYLS-QDGSFYFLELNPRLOQVHEPTTEMADVNDLP 457

379 AAOQLQVAMGPIYSIRDITRLYGMDPRGNEVIDFDSPSPESFKTQRKPPQGHVVACRIT 438

458 AAOQLQATAMGPIFLRIKDIRMVGVSPPMGDAPIDFENSA-----HVPKPRGHVIAARIT 510

439 AENPDPTGFKPGMGALTELNFRSSTTWGYSVGTSGALHEYADSQFGHIYAGGADRBSAR 498

511 SENPDEGFKPSGTVQVELNFRSNKNVNGYFSVAAAGGLHFPADSQFGHCFSGWENREBAI 570

499 KQMVISIKELSIKRGDFTTVEYLIIKLETFAPESNKLTGWLGLQIDRLTAERPAPDLA 558

571 SNMVALKELSIKRGDFTTVEYLIIKLETESFQNLRIDTGLDLRIAEKVQAEPRDPTWLG 630

559 V 559

631 V 631

RESULT 7

S41121

acetyl-CoA carboxylase (EC 6.4.1.2) - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2002

C;Accession: S41121

R;Ha, J.; Daniel, S.; Kong, I.-S.; Park, C.K.; Tae, H.J.; Kim, K.H.

Eur. J. Biochem. 219, 297-306, 1994

A;Title: Cloning of human acetyl-CoA carboxylase cDNA.

A;Reference number: S41121; MUID:94119704; PMID:7905825

A;Accession: S41121

A;Molecule type: mRNA

A;Residues: 1-2339 <HAJ>

A;Cross-references: UNIPARC:UPI000011EDFS; EMBL:X68968; NID:G452315; PIDN:CAA48770.1; I

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin

C;Keywords: biotin binding; ligase

F;120-620/Domain: biotin carboxylase homology <BCH>

F;747-819/Domain: lipoyl/biotin-binding homology <LPB>

F;786/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 61.3%; Score 1782; DB 2; Length 2339;

Best Local Similarity. 63.6%; Pred. No. 4.4e-118;

Matches 344; Conservative 78; Mismatches 105; Indels 14; Gaps 5;

QY 22 ASPVADPIRQGGHSHVITKVLICNNGLAANKVEIRSKWAYETFGDERAIEFTVMATPED 81

Db 103 ASP-AEFVTRPGNKVIEKVLINAGIAVYKMSRIRWSYEMFRNERAIRFVVMVTPED 161

82 LKVNADYIRMAOQYVEVPGSGNNNNYANVDLIVDVAERAGVHVAWAGWGHASENPRLPES 141

162 LKNAEYIKMADHYVPVPGGANNNNYANVELIIDIAKRIIPVQAVWAGWGHASENPKLP 221

142 LAASKHKLIIFPGPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKIKETWMSD---QGFL 198

Db 222 LL--KNGIAPMGPPSQAMWALGDKIASSIVAOAGIPTLPWSSGLRVDNQENDFSKRIL 279

QY 199 TVSDDDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKIRKCTNGBEFKOLYNALVG 258

Db 280 NVPQELYEKGYKVDVDDGLKAAEKVGYPMIKASEGGGKIRKVNADDFFNLFQVQA 339

QY 259 EYVPGSPVFMKLAGOARHLEVLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPED 318

Db 340 EYVPGSPVFMKLAGOARHLEVLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPED 399

QY 319 ARSEMEKAARLAKLVGVYSAGTVEWLYSPESGEPAFLNPLRQVHEHPTTEMVSGVNI 378

Db 400 VFEHMEQCAVKLAKWGVYSAGTVEYLYS-QDGSFYFLELNPRLQVHEHPTTEMVADNLP 458

QY 379 AAQLQVAMGPIPLYSIRDIRTLXGMDPRGNEVIDDFSSPESFKTKRQPOQGHVACRIT 438

Db 459 AAQLQVAMGPIPLYSIRDIRTLXGMDPRGNEVIDDFSSPESFKTKRQPOQGHVACRIT 511

QY 439 AENPDGTFKPGMGALTELNFRSSTWTGYSFVGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 512 SENPDGTFKPGMGALTELNFRSSTWTGYSFVGTSGALHEYADSQFGHIFAYGADRSEAR 571

QY 499 KQWVLSKELSGRDFRTTVEYLKLETDAPESNKITTCGLDGLIQRDLTAERPPADLA 558

Db 572 SNMVVALKELSGRDFRTTVEYLKLETDAPESNKITTCGLDGLIQRDLTAERPPADLA 631

QY 559 V 559

Db 632 V 632

RESULT 8

I38928

A;Map position: 17q12

A;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

F;120-620/Domain: biotin binding; ligase; liver

F;747-819/Domain: lipoyl/biotin-binding homology <BCH>

F;786/Binding site: biotin (lys) (covalent) #status predicted

Query Match 61.3%; Score 1781; DB 2; Length 2346;

Best Local Similarity 63.6%; Pred. No. 5.2e-118;

Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

QY 22 ASPVADPIRQOGSHSVITKVLICNNGIAAVERKIRKWAYETFGDERAIEFTVMTAPED 81

Db 103 ASP-AEFTVTRFGNRIKVLNNGIAAVERKIRKWAYETFGDERAIEFTVMTAPED 161

QY 82 LKYNADYIRMAQYVEVPGGNNNNYANVDLIIVDVAERAGVHVAWAGHASENPLPES 141

Db 162 LKANAETIKWADHYVPGGNNNNYANVDLIIVDVAERAGVHVAWAGHASENPKLP 221

QY 142 LAASKHKIIFIPGPGSARSLGDKISSTIVIAQHADVPKMPWSGTGKETWMSD---QGFL 198

Db 222 LL--KNGIAPMGPPSQAMWALGDKIASSIVAOAGIPTLPWSSGLRVDNQENDFSKRIL 279

QY 199 TVSDDDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKIRKCTNGBEFKOLYNALVG 258

Db 280 NVPQELYEKGYKVDVDDGLKAAEKVGYPMIKASEGGGKIRKVNADDFFNLFQVQA 339

QY 259 EYVPGSPVFMKLAGOARHLEVLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPED 318

Db 340 EYVPGSPVFMKLAGOARHLEVLADQYGNALISIFGRDCSVQRRHQKIIIEEAPVTIAPED 399

QY 319 ARSEMEKAARLAKLVGVYSAGTVEWLYSPESGEPAFLNPLRQVHEHPTTEMVSGVNI 378

Db 400 VFEHMEQCAVKLAKWGVYSAGTVEYLYS-QDGSFYFLELNPRLQVHEHPTTEMVADNLP 458

QY 379 AAQLQVAMGPIPLYSIRDIRTLXGMDPRGNEVIDDFSSPESFKTKRQPOQGHVACRIT 438

Db 459 AAQLQVAMGPIPLYSIRDIRTLXGMDPRGNEVIDDFSSPESFKTKRQPOQGHVACRIT 511

QY 439 AENPDGTFKPGMGALTELNFRSSTWTGYSFVGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 512 SENPDGTFKPGMGALTELNFRSSTWTGYSFVGTSGALHEYADSQFGHIFAYGADRSEAR 571

QY 499 KQWVLSKELSGRDFRTTVEYLKLETDAPESNKITTCGLDGLIQRDLTAERPPADLA 558

Db 572 SNMVVALKELSGRDFRTTVEYLKLETDAPESNKITTCGLDGLIQRDLTAERPPADLA 631

QY 559 V 559

Db 632 V 632

RESULT 9

A29924

acetyl-CoA carboxylase (EC 6.4.1.2), hepatic - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A29924; A29937; A27903

R;Takai, T.; Yokoyama, C.; Wada, K.; Tanabe, T.

J. Biol. Chem. 263, 2651-2657, 1988

A;Title: Primary structure of chicken liver acetyl-CoA carboxylase deduced from cDNA s

A;Reference number: A29924; MUID:88139305; PMID:2893793

A;Accession: A29924

A;Molecule type: mRNA

A;Residues: 1-2324 <TA1>

A;Cross-references: UNIPROT:P11029; UNIPARC:UPI0000127CAB; GB:J03541; NID:G211567; PID

R;Takai, T.; Wada, K.; Tanabe, T.

FEBS Lett. 212, 98-102, 1987

A;Title: Primary structure of the biotin-binding site of chicken liver acetyl-CoA carb

A;Reference number: A91375; MUID:87106011; PMID:2879745

A;Accession: A29337

A;Molecule type: mRNA

A;Residues: 493-820 <TA2>

A;Cross-references: UNIPARC:UPI0000171282; GB:X05019; NID:G63021; PIDN:CAA28675.1; PID

A;Accession: A27903

A;Molecule type: mRNA

A;Residues: 493-552, 554-783, 'RSPS', 789-820 <TA3>

A;Cross-references: UNIPARC:UPI000017312E

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti-

C;Keywords: biotin binding; ligase; liver

F;120-620/Domain: biotin carboxylase homology <BCH>

F;747-819/Domain: lipoyl/biotin-binding homology <LPB>

F;786/Binding site: biotin (lys) (covalent) #status predicted

Query Match 61.2%; Score 1780; DB 1; Length 2324;

Best Local Similarity 63.4%; Pred. No. 6e-119;

Matches 343; Conservative 81; Mismatches 103; Indels 14; Gaps 5;

QY 22 ASPVADPIRQOGSHSVITKVLICNNGIAAVERKIRKWAYETFGDERAIEFTVMTAPED 81

Db 103 ASP-AEFTVTRFGNRIKVLNNGIAAVERKIRKWAYETFGDERAIEFTVMTAPED 161

QY 82 LKYNADYIRMAQYVEVPGGNNNNYANVDLIIVDVAERAGVHVAWAGHASENPLPES 141

Db 162 LKANAETIKWADHYVPGGNNNNYANVDLIIVDVAERAGVHVAWAGHASENPKLP 221

F;615-687/Domain: lipoyl/biotin-binding homology <LPB>
F;654/Binding site: biotin (lys) (covalent) #status predicted

Query Match 60.4%; Score 1754.5; DB 2; Length 2123;
Best Local Similarity 65.2%; Pred. No. 3.4e-116;
Matches 326; Conservative 78; Mismatches 85; Indels 11; Gaps 3;

QY 54 IRSIRKWAYETFGDERAIEFTVMATPEDIKVNADYIRMAQDYVEVPGSGNNNNYANVDLI 113
DB 1 MRSIRKWAYETTFNDEKIIIOFVVMATPDDLHANSEYIRMAQDYVQVPGGTNNNNYANIDLI 60
QY 114 VDVAERAGYHVMAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQ 173
DB 61 LDVAEQTDVDAWAGWGHASENPELPALLASSQKILFIGPPGRAMRSLGDKISSTIVAQ 120
QY 174 HADVPQWMSGTGIGKTTMSDQ--GFLTYSDDVYQACIHTABEGLKAKBKIGYVPMIKA 231
DB 121 SAKIPCIPWSSGSHI-DTIHIDNKTNFVSPDDVYVRGCCSSPEDALEKAKLIGFVPMIKA 179
QY 232 SEGCGGKGRKCTNGEEFKQYNALVGEYGPSPVFYVWKLQAGQARHLEVQLLADQYGN AIS 291
DB 180 SEGCGGKGRVVDNEDDIFALYRQAVNETPGSPFMKVVTVDARHLEVQLLADQYGNIT 239
QY 292 IFGRDCSVORRHQKIIIEEAPVTIAPEDARESEKAAVRLAKLVGYYSAGTVEWLYSPESG 351
DB 240 LFGDCSIIQRHQKIIIEEAPVTITKETFORMERAIRLGEVGYYSAGTVEWLYSPKDD 299
QY 352 EFAPLEINRLQVHEHTTEMVSGVNIPTAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVID 411
DB 300 KFVFLINRLQVHEHTTEMISGVNLPATQLQIANGIPMHMISDIRKLYGLDPTGTSYID 359
QY 412 FDFSSPESFKTKQKPOQGHVAVCAITAEPNPDGFKPGMGALTELFNRSSTSTWGYFSVG 471
DB 360 -----FNKLKRPKPGKHCISCRITSEDPNDSGFKPSTGKIHELAFRSSNWNVGYFSVG 411
QY 472 TSGALHEYADSQFGHIFAYGADRSEARKQWVILSKELSIKSGDFRTTVEYILKLETD AFE 531
DB 412 NNGAIHSPDSQFGHIFAYGVNDQDAKQNVMLALKQFSIRGEFKTPIEYILLELETRDFE 471
QY 532 SNKITTGWLDGLIQDRLTAE 551
DB 472 SNNISTGWLDDLLKKNLSSD 491

RESULT 11
T07923
acetyl-CoA carboxylase (EC 6.4.1.2) A - rape (fragment)
C:Species: Brassica napus (rape)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T07923
R;Schulte, W.; Toepfer, R.; Stracke, R.; Schell, J.; Martini, N.
Proc. Natl. Acad. Sci. U.S.A. 94, 3465-3470, 1997
A:Title: Multi-functional acetyl-coenzyme A carboxylase from Brassica napus is encoded
A:Reference number: Z16220; MUID:97250561; PMID:9096417
A:Accession: T07923
A:Status: preliminary; translated from GB/EMBL/DBDB
A:Molecule type: DNA
A:Residues: 1-640 <SCH>
A:Cross-references: UNIPROT:O04849; UNIPARC:UPI000000A13BD; EMBL:Y10301; NID:g1934749; i
A:Experimental source: cv. Akela
C:Genetics:
A:Introns: 111/3; 180/3; 234/3; 265/3; 297/3; 355/3; 387/1; 449/3; 466/3; 480/1; 521/3;
C:Function:
A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A:Pathway: fatty acid biosynthesis
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C:Keywords: Cytozol; ligase
F;36-542/Domain: biotin Carboxylase homology <BCH>

Query Match 55.0%; Score 1598.5; DB 2; Length 640;
Best Local Similarity 53.9%; Pred. No. 7.6e-106;
Matches 306; Conservative 92; Mismatches 137; Indels 33; Gaps 5;

Db 81 EDNRINAEHRIADQFVEVPGTNNYVANNVQLLEIAETHVDVAVPGWGHASENP 140
QY 140 ESLSAASHKHIFITGPPGSMRSLGDKISSTIVAOHADVPCMPWGTGKTMDSQGLT 199
Db 141 DALKAK--GIVFLGPPAISMALGDKIGSSLIQAQAEVPTLPWSGSHVKIPPSD--LIT 196
QY 200 VSDVYOQACIHTAEGLKAEKIGYPMIKASGGGKGIKCTGEEFKQLYNVLCGE 259
Db 197 IPDEIYRAACVYITEEAIASQVVGYPAMIKASGGGKGIKRVHNDDEVRALFKVQGE 256
QY 260 VPSPVPMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRHKKIIEAPVTIAPEDA 319
Db 257 VPSPVPMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRHKKIIEAPVTIAPEDA 316
QY 320 RESNEKAAVRLAKLVGYVAGTVEWLYSPESGEFAFLELNPRLQVEHPPTMVGWVIPA 379
Db 317 VKSLEQAARLAKSVNYVGAATVEYLYSMETGEYFLELNPRLQVEHPPTMVGWVIPA 376
QY 380 AQLQVAMGIPLYSIRDTIRLYGMDPRGNE-----VIDEFSSPESFETKQKPOQ 430
Db 377 AQLQVAMGIPLYSIRDTIRLYGMDPRGNE-----VIDEFSSPESFETKQKPOQ 430
QY 431 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFVGTSGALHEYADSOFGHIFAY 490
Db 431 HCVAVRVTSDDPGTPTGKQVQLSFKSPKNWYFVSKGGGHEFSDSFGHVFAP 490
QY 491 GADRSEARKQWVLSKELSTRGDFRTTVEYLKLELTDAPESNKITTWGLDGLIQRDLTA 550
Db 491 GESRALAIANNVLGLKEIQIRGEIRTVNDVTIDILNASDYRDNKIHTWGLDSRIAMRVRA 550
QY 551 ERPPADLAV 559
Db 551 ERPPWYLSV 559

RESULT 16
T06161
N:Alternate names: acetyl-coenzyme A carboxylase
C:Species: Triticum aestivum (common wheat)
C:Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text_change 09-Jul-2004
R:Gornicki, P.; Faris, J.; Podkowinski, J.; Gill, B.; Haselkorn, R.
Proc. Natl. Acad. Sci. U.S.A. 94, 14179-14184, 1997
A:Title: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by a single
A:Reference number: Z15495; MUID:98054381; PMID:9391173
A:Accession: T06161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2311 <GOR1>
A:Cross-references: UNIPROT:O48959; UNIPARC:UPI00000A9808; EMBL:AF029895; NID:G2827149;
A:Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings
A:Accession: T06162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10, 'P', 12-67, 'H', 69-502, 'T', 504-619 <GOR2>
A:Cross-references: UNIPARC:UPI00000A5F07; EMBL:AF029897; NID:G2827153; PIDN:AAC39332.1;
A:Experimental source: cv. Hard Red Winter Tam 107, light-grown seedling
R:Elborough, K.M.; Simon, J.W.; Swinhoe, R.; Ashton, A.R.; Slabas, A.R.
Plant Mol. Biol. 24, 21-34, 1994
A:Title: Studies on wheat acetyl CoA carboxylase and the cloning of a partial cDNA.
A:Reference number: S42660; MUID:94154234; PMID:7906561
A:Accession: S42660
A:Molecule type: mRNA
A:Residues: 'WRTYM', 1771-2026, 'K', 2028-2073, 'F', 2075-2108, 'V', 2110-2120, 'L', 2122, 'A', 212
A:Cross-references: UNIPARC:UPI00000AABB05; EMBL:Z23038; NID:G396278; PIDN:CAA80573.1; PI
A:Molecule type: protein
A:Accession: S78600
A:Residues: 1847-1852, 'E', 1854-1863, 1947-1962, 'D', 1964; 2085-2091, 'HL', 2139-2155, 'I', 2157
A:Cross-references: UNIPARC:UPI00001552CB; UNIPARC:UPI00001552CD; UNIPARC:UPI000017627F;
C:Genetics:
A:Gene: ACC-1

A:Introns: 69/1; 90/2; 209/3; 278/3; 332/3; 363/3; 395/3; 453/3; 485/1; 547/3; 564/3;
C:Function:
A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A:Pathway: fatty acid biosynthesis
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C:Keywords: ligase
F:134-640/Domain: biotin carboxylase homology <BCH>
F:767-839/Domain: lipoyl/biotin-binding homology <LPB>
F:806/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 54.0%; Score 1569.5; DB 2; Length 2311;
Best Local Similarity 54.0%; Pred. No. 5.8e-103;
Matches 297; Conservative 95; Mismatches 137; Indels 21; Gaps 5;

QY 20 APASPVDPIRQGGHSHVTKVLCNNGIAAATVEIKRWAYETFGDERAIEFTVWATP 79
Db 114 ASLSKVVEFCMALGGKTPHSLVANNNGMAAAKFMESVETWNETFGSEKAIQLIAMATP 173
QY 80 EDLKNADYIRMDQVVEVPGGNNNNYANVDLIIVDAERAGVHVAWAGHASENRLP 139
Db 174 EDMRNAEHIRADQVVEVPGGNNNNYANVDLIIVDAERAGVHVAWAGHASENRLP 233
QY 140 ESLSAASHKHIFITGPPGSMRSLGDKISSTIVAOHADVPCMPWGTGK---ETWMSDQ 196
Db 234 DALNA--NGIVFLGPPSSMNLGDKVGSALLTAQAAGVPTLPWSGQVPEIPLEVCID--- 288
QY 197 FUTVSDVYQACIHTAEGLKAEKIGYPMIKASGGGKGIKCTGEEFKQLYNV 256
Db 289 --SIPAEYRKACVSTTEBALASQCMIGYPMIKASGGGKGIKCTGEEFKQLYNV 346
QY 257 LGEVPGSPVPMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRHKKIIEAPVTIAP 316
Db 347 QGEVPGSPVPMKLAGQARHLEVQLLADQYGNASIFGRDCSVQRHKKIIEAPVTIAP 406
QY 317 EDARESMKAAVRLAKLVGYVAGTVEWLYSPESGEFAFLELNPRLQVEHPPTMVGWV 376
Db 407 RETVKEQAARLAKLVGYVAGTVEWLYSPESGEFAFLELNPRLQVEHPPTMVGWV 466
QY 377 IPAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVIDFD-----FSSPSFETKQKPOQ 429
Db 467 LPAAQVAVGMGIPVQVPEIRRFYGMNDGGG---YDIWRKTAALATPFDVDSQWPK 522
QY 430 GHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFVGTSGALHEYADSOFGHIF 489
Db 523 GHCVAVRTSDDPGTPTGKQVQLSFKSPKNWYFVSKGGGHEFSDSFGHVF 582
QY 490 YGADRSEARKQWVLSKELSTRGDFRTTVEYLKLELTDAPESNKITTWGLDGLIQRDLT 549
Db 583 YGVSRAAATNMSLAKELIQIRGEIRTVNDVTIDILNASDYRDNKIHTWGLDSRIAMRV 642
QY 550 ERPPADLAV 559
Db 643 ERPPWYLSV 652

RESULT 17
A57710
acetyl-CoA carboxylase (EC 6.4.1.2) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A57710
R:Gornicki, P.; Podkowinski, J.; Scappino, L.A.; DiMaio, J.; Ward, E.; Haselkorn, R.
Proc. Natl. Acad. Sci. U.S.A. 94, 6860-6864, 1994
A:Title: Wheat acetyl-Coenzyme A carboxylase: cDNA and protein structure.
A:Reference number: A57710; MUID:94316597; PMID:7913745
A:Accession: A57710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2257 <GOR>
A:Cross-references: UNIPROT:O41511; UNIPARC:UPI00000A8884; GB:U010187; NID:G514305; PIDN
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C:Keywords: ligase
F:29-534/Domain: biotin carboxylase homology <BCH>

[illegible]

A; Experimental source: strain Williams 82; leaf

A; Experiment

central source: st:

rain Williams 82; leat

C:Genetics:

A:Gene: ACCase-B
 A:Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 391/3; 454/3; 471/3; 484/3; 526/3;
 5/3; 1464/3; 1524/3
 C:Function:
 A:Description: catalyzes ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
 A:Pathway: fatty acid biosynthesis
 C:Superfamily: human acetyl-CoA carboxylase
 C:Keywords: ligase
 F:41-547/Domain: biotin carboxylase homology <BCH>
 F:674-746/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 53.5%; Score 1555.5; DB 2; Length 1978;
 Best Local Similarity 53.2%; Pred. No. 4.6e-102;
 Matches 291; Conservative 100; Mismatches 141; Indels 15; Gaps 4;

QY 20 APASPVADIRKQGGHSHVTKVLCNNGIAAVERKIRKWAYETFGDERAIEFTWATP 79
 DB 21 AAISEVDDFCNALCGNRPISILIANNGMAAVKPIRSVRSWAYETFGSEKAILLVAMATP 80
 QY 80 EDLKNVADYIRMAQOVVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPLP 139
 DB 81 EDWRIINAEHRIADQFAEVPGGTNNNNYANVQLILEMAETHYDVAVPGWGHASENPEL 140
 QY 140 ESLSAASKHKIIFIGPPGSAWRSGLDKISITVAQHADVPMPWSGTGKIKETMMSDQGLT 199
 DB 141 DALKAK--GIVFLGPPAISMAALODKIGSLIAQAQAEVPTLPWSGSHVK--IPPESSLIT 196
 QY 200 VSDVYVQQAQCIHTAEBGLEKAEKIGYPVMIKASGGGGKIRKCTNGEEFKQLYNALVGE 259
 DB 197 IPDEIVREACVYTTTEAVASQVVGYPAMIKASWGGGKIRKVNHNDEVRALFKQVQGE 256
 QY 260 VPGSPVPVVKLAQARHLEVQLLADQVGNALISIFGRDCSVORRHOKIIEBAPVTIAPEDA 319
 DB 257 VPGSPPIFMKVASQSRHLEVQLLADQVGNALISIFGRDCSVORRHOKIIEBAPVTIAPET 316
 QY 320 RESMEKAAVRLAKLVGVSGAGTVEWLYSPESGFAFLELNPRQLQVEHPVTTEWIAEVA 379
 DB 317 VQLEQAARRLAKSVNYVGNATVEYLFVSMETGYFLELNPRQLQVEHPVTTEWIAEVA 376
 QY 380 AQLQVAMGPIYSIRDITLYGMDPRGNEVIDFD-----FSSPESFKTORPQPGHV 432
 DB 377 AQVAIGMGIPLWQIPEIRRFYVGHGG---YDAWRKTSVLATPFDKQAQSTRPKGHC 432
 QY 433 VACRIATNPDTGFKGCMGALTINFRSTSTWGYFSGTSGALHAYVADSQFGHIFAYGA 492
 DB 433 VAVRVTSDDPDGFKPTSGKVQLSKPNVWAFSVKSGGGIHFEFSDQFGHVFAPGE 492
 QY 493 DRSEARKQWVLSKELSIKSGDRTTVEYLIKLETDFAFESNKITTCWLDGLIODRLTAER 552
 DB 493 SRAUTTANMVLGLKEIQIRGEIRNVDTYIDLLNASDYRENKHTGWLDSRIAMRVRAER 552
 QY 553 PPADLAV 559
 DB 553 PPWYLSV 559

RESULT 20

T02235
 N:Alternate names: acetyl-coenzyme A carboxylase
 C:Species: Zea mays (maize)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02235

R:Engl, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
 Plant Physiol. 108, 1299-1300, 1995

A:Title: A maize acetyl-coenzyme A carboxylase cDNA sequence.
 A:Reference number: Z14632; MUID:95357420; PMID:7630949

A:Accession: T02235

A:Status: preliminary; translated from GE/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-2325 <EGI>

A:Cross-references: UNIPROT:Q41743; UNIPARC:UPI00000A4B72; EMBL:U19183; NID:g1045304; PJ

A:Experimental source: strain A188; leaf

C:Function:

A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
 A:Pathway: fatty acid biosynthesis
 C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
 C:Keywords: ligase
 F:134-640/Domain: biotin carboxylase homology <BCH>
 F:767-839/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 53.1%; Score 1543.5; DB 2; Length 2325;
 Best Local Similarity 53.5%; Pred. No. 4.2e-101;
 Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;

QY 20 APASPVADIRKQGGHSHVTKVLCNNGIAAVERKIRKWAYETFGDERAIEFTWATP 79
 DB 114 ASVSKVFECAALGGKTPHISILVANNMGMAAKFMRSVETWANDTFGSEKAILLIAMATP 173
 QY 80 EDLKNVADYIRMAQOVVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPLP 139
 DB 174 EDMRINAEHRIADQFAEVPGGTNNNNYANVQLIVGMAQKLGVSAPWPGWGHASENPEL 233
 QY 140 ESLSAASKHKIIFIGPPGSAWRSGLDKISITVAQHADVPMPWSGTGKIKETMMSDQGLT 196
 DB 234 DALKAK--GIVFLGPPAISMAALODKIGVSALIAQAQAEVPTLPWSGSHVEVPLECCLD--- 288
 QY 197 FLTVDVYVQQAQCIHTAEBGLEKAEKIGYPVMIKASGGGGKIRKCTNGEEFKQLYNALV 256
 DB 289 --AIPEMYRKACVYTTTEAVASQVVGYPAMIKASWGGGKIRKVNHNDEVRALFKQV 346
 QY 257 LGEVPGSPVPVVKLAQARHLEVQLLADQVGNALISIFGRDCSVORRHOKIIEBAPVTIAP 316
 DB 347 QGEVPGSPPIFMKVASQSRHLEVQLLADQVGNALISIFGRDCSVORRHOKIIEBAPVTIAP 406
 QY 317 EDARESMEKAAVRLAKLVGVSGAGTVEWLYSPESGFAFLELNPRQLQVEHPVTTEWIAEVA 376
 DB 407 RETVKALEQAARRLAKAVGVGAATVEYLFVSMETGYFLELNPRQLQVEHPVTTEWIAEVA 466
 QY 377 IPAAQLQVAMGPIYSIRDITLYGMDPRGNEVIDFD-----FSSPESFKTORPQPGHV 429
 DB 467 LPAAQVAVGMGIPLWQIPEIRRFYVGHGG---YDIWRKTAALATPFDKQAQSTRPKGHC 522
 QY 430 GHVACRIATNPDTGFKGCMGALTINFRSTSTWGYFSGTSGALHAYVADSQFGHIFAYGA 489
 DB 523 GHCVAVRTISDDPDGFKPTSGKVQLSKPNVWAFSVKSGGGIHFEFSDQFGHVFAPGE 582
 QY 490 YGADRSEARKQWVLSKELSIKSGDRTTVEYLIKLETDFAFESNKITTCWLDGLIODRLTAER 549
 DB 583 YGLSRPAALITNMSLAKELIQIRGEIRNVDTYIDLLNASDYRENKHTGWLDSRIAMRVQ 642
 QY 550 AERPPADLAV 559
 DB 643 AERPPWYLSV 652

RESULT 21

A48757

acetyl-CoA carboxylase (EC 6.4.1.2) - Cyclotella cryptica

C:Species: Cyclotella cryptica

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A48757

R:Roessler, P.G.; Ohlrogge, J.B.

J. Biol. Chem. 268, 19254-19259, 1993

A:Title: Cloning and characterization of the gene that encodes acetyl-coenzyme A carboxylase

A:Reference number: A48757; MUID:93374903; PMID:8103514

A:Accession: A48757

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-2089 <ROE>

A:Cross-references: UNIPROT:Q39478; UNIPARC:UPI00000A5A26; GB:I20784; NID:g1065903; PII

A:Note: authors translated the codon GGC for residue 1834 as Ala

C:Genetics:

A:Introns: 25/1; 729/1

C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin

A;Accession: J32413
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-2054 <GOE>
A;Cross-references: UNIPROT:Q9G1I3; UNIPARC:UPI00000075897; EMBL:AF025469; PIDN:RAB71048.
A;Experimental source: strain Bristol N2; clone W09B6
C;Genetics:
A;Gene: CESP:W09B6.1
A;Map position: 2
A;Introns: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C;Keywords: liqase

Qy. 22 ASPVADFIRKQGHSVITKVLI CNNGIAA VKEIRSINKWAYETFGDERAIEFTVMATPED 81
:: :: :: | : :: | : : | : : | : : | : : | : : | : : | : : | : : | : :
Dp 14 SNKTDFVMMJEGRSIKRIIVANNGIAAMKCLISROWLONOGTSGVVSVFCIATEDE 73

RESULT 26

AH1923
biotin carboxylase [imported] - Nostoc sp. (strain PCC 7120)
A;Accession: A53311
C;Species: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1923
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimizu, N.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH1923
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <KUR>
A;Cross-references: UNIPROT:Q06862; UNIPARC:UPI00001251AA; GB:BA000019; PIDN:BA072896.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: accC
C;Superfamily: biotin carboxylase; biotin carboxylase homology

Query Match 24.4%; Score 709.5; DB 2; Length 447;
Best Local Similarity 32.9%; Pred. No. 9e-43;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

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Qy 40 KVLICNNGIAAVKEIRSKWYETFGDERAIEFTVMATPDLKVNADYIRMAOYVEVP 99
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53
Qy 100 GGSNNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAALTRNASAIHPGYFLSENAKFAEICA--DHIIAFIGTPEAI 111
Qy 160 RSLGDKISSTIVAQHADVPICMPWSGTGKETMMSDQGLTVDVYQQACIHTAEGLK 219
Db 112 RLMGDKSTAKETWKAGVTPVGS-----EGLVETEQEGLEL 148
Qy 220 AEKIGYPMVKASGEGGGKIRKCTNGEBEPKQLYNAVLEGEV-----PGSPVFMKLAGOAR 275
Db 149 AKDIGYPMVKATAGGGGRMLVRSPDEFVKFLFLAAQGEAGAAFGNAGVYIEKFIERPR 208
Qy 276 HLEVQLLADQGNNAISIFGRDCSVORRHOKIIEAPVTIAPEDARESMKAAVRLAKLVG 335
Db 209 HIEFQILADNNGVNHIGERDCSIOQRNQLKEEAPSPALDSUREKMGQAAVRAAQFIN 268
Qy 336 YVSAGTVEWLYSPESGEFAFLNPRLOVEHPHTTMMVSGVNIIPAAQLQVAMGIPLYSIRD 395
Db 269 YTGAGTIEFLD-RSGQFYFEMNTRIQLVEHPVTMTVGVDDLVEQIRIAQGERLRLTQD 327
Qy 396 IRTLYGMDPRGNEVIDPFPSSPESFKTQKPOQGHVVACRITAEINPDGFKPGMGALTE 455
Db 328 QVWL-----RGHAIECRINAEDPDHDFRPAPGRIS- 357
Qy 456 LNFRSSTWGVSVGTSGA-----LHEYADSOFGHIIFAYGADRSEARKQWVIS 504
Db 358 -----GYLPPGGGVIRIDSHVYTDYQIIPYDLSLIGLIVMGDPDRATINRMKRA 407
Qy 505 LKELSGIRGDFRTTVEYLKLETFDAFESNKITTWGL 540
Db 408 LRECAITG-LPTTIGFQHRIMENPQFLQGNVSTSFV 442
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RESULT 27

A53311
biotin carboxylase (EC 6.3.4.14) - Anabaena sp. (strain PCC 7120)
N;Alternate names: acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase chain
C;Species: Anabaena sp.
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: A53311
R;Gornicki, P.; Scappino, L.A.; Haselkorn, R.
J. Bacteriol. 175, 5268-5272, 1993

A;Title: Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. strain
A;Reference number: A53311; MUID:93352435; PMID:8102363
A;Accession: A53311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <GOR>
A;Cross-references: UNIPROT:Q06862; UNIPARC:UPI00001251AA; GB:L14862; NID:g289132; PIDN
C;Superfamily: biotin carboxylase; biotin carboxylase homology
C;Keywords: ATP; ligase
F;5-447/Domain: biotin carboxylase homology <BCH>

Query Match 24.4%; Score 709.5; DB 2; Length 447;
Best Local Similarity 32.9%; Pred. No. 9e-43;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

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Qy 40 KVLICNNGIAAVKEIRSKWYETFGDERAIEFTVMATPDLKVNADYIRMAOYVEVP 99
Db 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53
Qy 100 GGSNNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAALTRNASAIHPGYFLSENAKFAEICA--DHIIAFIGTPEAI 111
Qy 160 RSLGDKISSTIVAQHADVPICMPWSGTGKETMMSDQGLTVDVYQQACIHTAEGLK 219
Db 112 RLMGDKSTAKETWKAGVTPVGS-----EGLVETEQEGLEL 148
Qy 220 AEKIGYPMVKASGEGGGKIRKCTNGEBEPKQLYNAVLEGEV-----PGSPVFMKLAGOAR 275
Db 149 AKDIGYPMVKATAGGGGRMLVRSPDEFVKFLFLAAQGEAGAAFGNAGVYIEKFIERPR 208
Qy 276 HLEVQLLADQGNNAISIFGRDCSVORRHOKIIEAPVTIAPEDARESMKAAVRLAKLVG 335
Db 209 HIEFQILADNNGVNHIGERDCSIOQRNQLKEEAPSPALDSUREKMGQAAVRAAQFIN 268
Qy 336 YVSAGTVEWLYSPESGEFAFLNPRLOVEHPHTTMMVSGVNIIPAAQLQVAMGIPLYSIRD 395
Db 269 YTGAGTIEFLD-RSGQFYFEMNTRIQLVEHPVTMTVGVDDLVEQIRIAQGERLRLTQD 327
Qy 396 IRTLYGMDPRGNEVIDPFPSSPESFKTQKPOQGHVVACRITAEINPDGFKPGMGALTE 455
Db 328 QVWL-----RGHAIECRINAEDPDHDFRPAPGRIS- 357
Qy 456 LNFRSSTWGVSVGTSGA-----LHEYADSOFGHIIFAYGADRSEARKQWVIS 504
Db 358 -----GYLPPGGGVIRIDSHVYTDYQIIPYDLSLIGLIVMGDPDRATINRMKRA 407
Qy 505 LKELSGIRGDFRTTVEYLKLETFDAFESNKITTWGL 540
Db 408 LRECAITG-LPTTIGFQHRIMENPQFLQGNVSTSFV 442
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RESULT 28

H81978
probable acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxylase chain NMA0596 [similar:
N;Contains: biotin carboxylase (EC 6.3.4.14)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: H81978
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori
Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A;Reference number: AB1775; MUID:20222556; PMID:10761919
A;Accession: H81978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <PAR>
A;Cross-references: UNIPROT:Q9JW07; UNIPARC:UPI00000C49E5; GB:AL162753; GB:AL157959; N
C;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: accC; NMA0596
C;Superfamily: biotin carboxylase; biotin carboxylase homology

C;Keywords: ligase

Query Match 23.4%; Score 679; DB 2; Length 453;
Best Local Similarity 32.6%; Pred. No. 1.4e-40;
Matches 170; Conservative 90; Mismatches 176; Indels 86; Gaps 13;
Matches 170; Conservative 90; Mismatches 176; Indels 86; Gaps 13;
QY 37 VITKVLICNNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMAQYV 96
DB 1 MLKKVLIANRGEIAVLRLACRENGIAT-----VAVHSEADKDSLHVKLADSV 49
QY 97 EYVPGSGNNNNYANVDLIVDAERAGVHVAWGCHASENPRLPSLAASKHKIIFIPGPG 156
DB 50 CIGPAASQAQSYINPAIAAAEVSADAVHPGYGFLAENADFAEQVQS--GFTFIGPKP 107
QY 157 SAMSLGDKISSTIVAHADVPMPWSGTGKETMMSDQGLTVSDDDVYQACIHTAEEG 216
DB 108 DTRLMGDKVSAKAMTAAGVPCVPGS-----DQALPDDG-----EEI 145
QY 217 LEKAEKIGYPVMIKASGGGGKIRKCTNGEEFKQ---LYNAVILGEVPGSP-VFVMKLAG 272
DB 146 LKIAKIGYPVILKASGGGGKIRVVEKKEDILQVSEMTKAEAGAFGNPMVYMERVLQ 205
QY 273 QARHLEVQLLADQVGNNAISIPGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRLAK 332
DB 206 RPRHVEIQVIADEHGNVLAERDCSLQRRHQKIEEAPVITEKERAKIGKACADACK 265
QY 333 LVGVVSAGTVMWLYSPSGEFAFLNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIP-L-Y 391
DB 266 RIGVRGAGTFFFLY--EDGEEFFIEMTRVQVEHPVTELITGVNDIVQEQRLAAGLPLQY 323
QY 392 SIRDITLYGMDPRGNEVIDPFFSSPESFKTORPQGHVACRITAENPDTGFKPGMG 451
DB 324 KQKDI-----QVEGAFECRINAEDP-YNFIPIPG 352
QY 452 ALTELNFRSTSTWGYVSGTSGALHE-----YADSQGHIFAYGADRSEARKQWISL 505
DB 353 PIESCHLPSPG-----FGIRVDSHIYGYRIPPYDYSILGKVCVVGKDRDQAMAKRVAL 406
QY 506 KELSIRGDFRTTVEYLKLETDAPESNKITTGWLDGLIQDR 547
DB 407 AELAITG-IKTNTPLRLDLPNDPGFQKGVSGIHYLEHLEDR 447

RESULT 29

A69581
acetyl-CoA carboxylase (biotin carboxylase subunit) accC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69581
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berth
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Toato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yara, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69581
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-450 <KUN>
A;Cross-references: UNIPROT:P49787; UNIPARC:UPI000000606EA; GB:Z59116; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: accC

C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;4-450/Domain: biotin carboxylase homology <BCH>

Query Match 23.3%; Score 676; DB 2; Length 450;
Best Local Similarity 33.2%; Pred. No. 2.2e-40;
Matches 172; Conservative 81; Mismatches 177; Indels 88; Gaps 12;
QY 37 VITKVLICNNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMAQYV 96
DB 1 MIKKVLIANRGEIAVLRIACRELGIET-----VAVSEADKDLHVQMADEAF 49
QY 97 EYVPGSGNNNNYANVDLIVDAERAGVHVAWGCHASENPRLPSLAASKHKIIFIPGPG 156
DB 50 CIGPKASKDSYLVNTVIVSAKLTGTDAIHPGVGFLAENADFAE--LCEEVNTVFGPSP 107
QY 157 SAMSLGDKISSTIVAHADVPMPWSGTGKETMMSDQGLTVSDDDVYQACIHTAEEG 216
DB 108 DAISKMGTKDVARETMKQAGVPIVPGS-----QGIIENVEEA 144
QY 217 LEKAEKIGYPVMIKASGGGGKIR-----KCTNGEEFKQLYNVILGEVPGSPVFMKL 270
DB 145 VSLANEIGYPVILKASGGGGKIRVARTEEELINGIKITQQAATAFRNPG--VYIEKY 202
QY 271 AGQARHLEVQLLADQVGNNAISIPGRDCSVQRRHQKIEEAPVTIAPEDARESMEKAAVRL 330
DB 203 IEDFRHVEIQVLADNTGNTIHLGERDCSQRRLKLLSPSPALDSEIREQMGDAVKA 262
QY 331 AKLVGVVSAGTVMWLYSPSGEFAFLNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIP-L 390
DB 263 AKAVGTGAGTVEFYIDYNEQRYFEMMNTRIQVEHPVTEMVTGTDLIKEQIKVASGMEL 322
QY 391 YSIRDITLYGMDPRGNEVIDPFFSSPESFKTORPQGHVACRITAENPDTGFKPGM 450
DB 323 -SLK-----QEDVEF-----EGWAIECRINAENSPSKNFMPS 353
QY 451 GALT-----ELNFRSTSTW-GYFSVGTSGALHEYADSOFGHIFAYGADRSEARKQW 503
DB 354 GRKMWLPGLGVRVDSAAVPGY-----SIPPYDYSIAKVIITYGKTRDRAIEMKR 406
QY 504 SKKELSIRGDFRTTVEYLKLETDAPESNKITTGWLD 541
DB 407 ALSEFVIEG-IETTIPFLKLEHETVSGEFNTEKLE 443

RESULT 30

D69277
biotin carboxylase (acc) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69277
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woose, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69277
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-506 <KLE>
A;Cross-references: UNIPROT:Q30019; UNIPARC:UPI00000571AD; GB:AE001090; GB:AE000782; N
C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;4-450/Domain: biotin carboxylase homology <BCH>

Query Match 23.2%; Score 675; DB 2; Length 506;
Best Local Similarity 33.7%; Pred. No. 3.1e-40;
Matches 180; Conservative 83; Mismatches 165; Indels 106; Gaps 18;
QY 37 VITKVLICNNNGIAAVKEIRSIRKWAYETFG-----DERAIEFTVMATPEDLKVNAD---Y 88
DB 1 MFSKLIIVNRGEIAVVRVWACHLGKIKTVGVSSADKRAFH-----RYVADCEY 50

QY 89 IRADQVVEPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHK 148
DB 51 IGRADP-----RDSYLNIDRIIEIVAKSGAEAIHPGYGFLAENAEFAE--RCEEEG 99
QY 149 IIFGPPGSAMRSLGDKISSTIVAHQADVPCMPWSGTGKETWMSDQGLTVSDVYQQA 208
DB 100 IVFPGSPFVIRTAGSKVRRESNQRAGVPVPGSPK-----136
QY 209 CIHTAEGLKAEKIGYPMIKASEGGGKIRKCTNGEEBFKQLY--NAVIGE--VPGSP 264
DB 137 -IDTVDEAKAEKIGYPMIKASEGGGKIRKCTNGEEBFKQLY--NAVIGE--VPGSP 264
QY 265 VFWMLAGQARHLEVOQLADQYGNASIFGRDCSVQRHOKITEEAPVTIAPEDARESME 324
DB 196 VYLEKYLARPHIEVOQLADQYGNASIFGRDCSVQRHOKITEEAPVTIAPEDARESME 324
QY 325 KAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLNPRLOVHEHPTTEMVSGVNPAAQLOV 384
DB 256 KLVKAGAREGYTNAGTFFELY--ENGNYFLEINSLOVHEHPTTEMVSGVNPAAQLOV 384
QY 385 AMGIPLYSIIRDTLYGMDPRGNEVIDFDFSSPESFKTKRQPOQGHVACRITAENPDT 444
DB 314 AYG-----EELR-----HGQEDVAI-----RGHAIECRINAEDP-V 343
QY 445 GFPGMGALTELPFRSSTSTWGYFSVGTSGALH-----EYADSOFGHIFAYGADRSEAR 498
DB 344 NFYPRSGRI--LHYRSP---GGIGIRVDSGIHMGYRIPEYDSMTSKLJAYGETREAI 397
QY 499 KOMVLSIKELSGDFRTTVEYLKLETDAPESNKITTCWLDGLIQDRLT 549
DB 398 ARMKRALYELIEG-VETNIPFPFAVLNDEFEVGNHTXFP-----VEERNIAEK 446
RESULT 31
S74380
biotin carboxylase accC - Synecocystis sp. (strain PCC 6803)
N/Alternate names: hypothetical protein sl10053
C/Species: Synecocystis sp.
A/Variety: PCC 6803
C/Accession: S74380
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S74380
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-448 <ARN>
A/Cross-references: UNIPROT:Q55160; UNIPARC:UPI0000003466; EMBL:D64001; GB:AB001339; NIH
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
A/Gene: accC
C/Superfamily: biotin carboxylase; biotin carboxylase homology
F;5-448/Domain: biotin carboxylase homology <BCH>
Query Match 23.1%; Score 671.5; DB 2; Length 448;
Best Local Similarity 31.8%; Pred. No. 4.6e-40;
Matches 167; Conservative 94; Mismatches 167; Indels 97; Gaps 12;
QY 40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPDLKVNADYIRMAQYVEP 99
DB 5 KILIANRGETALRIHSCEELGIPT-----VAVHSTIDRHALHVLANESVCIG 53
QY 100 GGNNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHKIIFGPPGSAM 159
DB 54 PPPSNKSYLNIPNIIAALATRNATAIHPGYGFLAENARFAICA--DHOITFGPSPEAI 111
QY 160 RSLGDKISSTIVAHQADVPCMPWSGTGKETWMSDQGLTVSDVYQQAACHTAEBGLEK 219

DB 112 TAMGDKSTAKTMQKSGVPCVPGS-----PGLIESEATALKI 148
QY 220 ABKIGYPMIKASEGGGKIRKCTNGEEBFKQLYNAVLEGPV---GSP-VFVNMKLAGQAR 275
DB 149 AAEIGYPMIIKATAGCGGRGMLVQBEKDFKLFLHAAQGEAGAAFGNPGVLEKFEKPR 208
QY 276 HLEVOQLADQYGNASIFGRDCSVQRHOKITEEAPVTIAPEDARESMEKAAVRLAKLVG 335
DB 209 HIEPQILADQYGNVHLGERDCSIQRHOKILEEAPSPFLTPHLRKKMGEEAAVKAASIN 268
QY 336 YVSAGTVEWLYSPESGEFAFLNPRLOVHEHPTTEMVSGVNPAAQLOVAMGIPLYSIRD 395
DB 269 YVGAGTVEFLVD--GNGNFYFEMWNTFIOVEHPVTEMITGYDLISEQIRIANG-----319
QY 396 IRTLYGMDPRGNEVIDFDFSSPESFKTKRQPOQGHVACRITAENPDTGFKPGMGALTE 455
DB 320 -----EKLRFQSDVEI-----RGHAIECRINAEDPKQNFRRHPGKIS- 357
QY 456 LNFRSSTSTWGYFSVGTSGA-----LHEYADSOFGHIFAYGADRSEARKOMVIS 504
DB 358 -----AYLPPGGVGRIDSHVYTYEIPPYDYSILGKLIWAGDRPSAIKRMQRA 407
QY 505 LKELSGRSGDFRTTVEYLKLETDAPESNKITTCWLDGLIQDRLT 549
DB 408 LRECAITG-VPTLEPHQRILOTPAFLAGDVYTNF-----IEEHLT 447
RESULT 32
G71860
biotin carboxylase - Helicobacter pylori (strain J99)
C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa
A/Reference number: A71800; MUID:99120357; PMID:9923682
A/Accession: G71860
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-455 <ARN>
A/Cross-references: UNIPROT:Q9ZK08; UNIPARC:UPI00000036D6; GB:AE001529; GB:AE001439; N
A/Experimental source: strain J99
C/Genetics:
A/Gene: accC
C/Superfamily: biotin carboxylase; biotin carboxylase homology
F;15-455/Domain: biotin carboxylase homology <BCH>
Query Match 23.0%; Score 668; DB 2; Length 455;
Best Local Similarity 32.3%; Pred. No. 8.3e-40;
Matches 166; Conservative 87; Mismatches 177; Indels 84; Gaps 11;
QY 38 ITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPDLKVNADYIRMAQYVE 97
DB 13 LSRILIANRGETALRIATQIQMGKES-----TAIYSIAKDRAHLYNTAKKVC 61
QY 98 VPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHKIIFGPPGS 157
DB 62 ICGAKSSESYLNIPALISAELFEADAIFPGYGFLENQNFVE--ICSHHSLEFIFGSAK 119
QY 158 AMRSLGDKISSTIVAHQADVPCMPWSGTGKETWMSDQGLTVSDVYQQAACHTAEBGL 217
DB 120 VVALMSDKAKAKIVKKEAGMPYIEGSDGLKS-----YQEA-----E 156
QY 218 EKAEGYPMIKASEGGGKIRKCTNGEEBFKQLYNA---VLGEVPGSPFVFMKLAGQ 273
DB 157 ETADKIGYPMIIKAAAGGGGRGMRVVGDSKULNLYLAETAETALSFAFGDGSVYLEFPIN 216
QY 274 ARHLEVOQLADQYGNASIFGRDCSVQRHOKITEEAPVTIAPEDARESMEKAAVRLAKL 333
DB 217 PHIEVOQLADQYGNVHLGERDCSVQRHOKILEEAPVLEESVYRKLELTAIKAKY 276

QY 334 VGVYAGTVEWLYSPSGEFAFLNPRLOVEHPTTEMVSGVNI PAAQLQVANGIPLYSI 393
Db 277 IGYVGAGTFEFLDSDNNKKDYFEMEMNTRLOVEHTISEMVSGLNLIEMWIKIAQGEEL--- 333
QY 394 RDITLYGMDPRGNEVIDDFSSPESFKTKQKPOQPOGHVACRITAENPDPTGFKPGMGAL 453
Db 334 -----PKQESFSL-----KGAIECRITAEADPKK-FYPSPGKI 365
QY 454 TE-----LNFRSTSTWGVSTGSGALHEYADSGFHIFAYGADRSEARKQWVLSLKE 507
Db 366 TEWIAFGVNVRLDSHAHNVVPTN-----YDSMIGKLVWGENREARAKWKAALKE 419
QY 508 LSIRGDFRTTVEYLKLETDAPESNKITGWLD 541
Db 420 FKVEG-IKTTIPPHIELENAEDFRQAKIHTKYLE 452

RESULT 33
F81033
acetyl-CoA carboxylase, biotin carboxylase NMB1861 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81033
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81033
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-453 <TET>
A:Cross-references: UNIPROT:O9JXW3; UNIPARC:UPI00000C47EE; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1861
C:Superfamily: biotin carboxylase; biotin carboxylase homology

Query Match 22.9%; Score 667; DB 2; Length 453;
Best Local Similarity 32.4%; Pred. No. 9.7e-40;
Matches 169; Conservative 90; Mismatches 177; Indels 86; Gaps 13;

QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYV 96
Db 1 MLKKVLIANRGETALRVLRACREMGAT-----VAVHSEADKOSLHVYKLADSV 49
QY 97 EYVGGNNNNYANVDLIVDAERAGVHAVWAGHASENPRLPESLAASKHKIIFIGPPG 156
Db 50 CIGPAASAQSYLVNPAIIAAAEVSCADAVHPGYGFLAENADFAEQVEQS--GFTFIGPKP 107
QY 157 SAMRSLGDKISSITVAQHADVPCMPWSGTGKETMMSDQGLTVSDVYQACIHTAEEG 216
Db 108 DTIRLMGDKVSAXHAIAGVPCVPS-----DQALPDQG-----EEI 145
QY 217 LEKAKIGYPMVKASGEGGKIRKCTNGEEFQK---LYNAVIGVPGSP-VFVMKLAG 272
Db 146 LKTIADKVGYPVILKASGGGGRGMRVVEKKEDLLQSVMTKAAAGAFGNPMYMYRLQ 205
QY 273 QARHLEVOLLADQYNAISIFGRDCSVQRHOKIIEEAPVTIAPEDARESMKAAVRLAK 332
Db 206 RPRHVEIQVIADSHGNAIYLAERDCSLQRHOKVIEEAPAFITEKERAKIGNACADACK 265
QY 333 LVGYVSAGTVEWLYSPSGEFAFLNPRLOVEHPTTEMVSGVNI PAAQLQVANGIPLY 391
Db 266 RIGYRGAGTPEFLY--EDGEFFIEMNTRVQVHPVTEITGVIVQEQRLIAAGLPLQY 323
QY 392 SIIRDITLYGMDPRGNEVIDDFSSPESFKTKQKPOQPOGHVACRITAENPDPTGFKPGMG 451
Db 324 KQKDI-----QVEGHAFECRINAEDP-VNFIIPSPG 352

QY 452 ALTELNFRSSTWGVSTGSGALHE-----YADSGFHIFAYGADRSEARKQWVLSL 505
Db 353 LI-----ESCHLPQGFIRVDSHIYQGVRIIPPYDLSLGIKICVHKTRQAMAKQVAL 406
QY 506 KELSIRGDFRTTVEYLKLETDAPESNKITGWLDGLIQDR 547
Db 407 AELAVTG-IKTTWPLRDLFADAGFKQGGVSIHLEHWLEDR 447

RESULT 34
G95929
probable methylcrotonoyl-CoA carboxylase (BC 6.4.1.4) [imported] - Sinorhizobium meli
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004
C:Accession: G95929
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing en
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95929
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-662 <KUR>
A:Cross-references: UNIPROT:O92VJ8; UNIPARC:UPI00000CB61A; GB:AL591985; PIDN:CAC49103.
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punlier, A.; Abola, P.; Ampe, F.; Barloy-Huble
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hymen, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaur
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: mccb; SMD21124
A:Genome: plasmid
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti
C:Keywords: ligase

Query Match 22.9%; Score 666; DB 2; Length 662;
Best Local Similarity 33.1%; Pred. No. 2e-39;
Matches 176; Conservative 84; Mismatches 195; Indels 76; Gaps 12;

QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYV 96
Db 1 MFSKLLIANRGETACRIITARRLGIRT-----VAVYSDADGDALHVALADEAI 49
QY 97 EYVGGNNNNYANVDLIVDAERAGVHAVWAGHASENPRLPESLAASKHKIIFIGPPG 156
Db 50 RIGGAPAAESYLASAPIVOAERSVGAQAIHPGYGFLSENADFAEVAEA--GMIFVGPFP 107
QY 157 SAMRSLGDKISSITVAQHADVPCMPWSGTGKETMMSDQGLTVSDVYQACIHTAEEG 216
Db 108 AAIRANGLKDAKALMERSGVPPV--GYHGE--QDASFLA----- 145
QY 217 LEKAKIGYPMVKASGEGGKIRKCTNGEFPKQLYNAVIGLVEPVS-----PVFVMKLAG 272
Db 146 -DRAREIGYPLIKARAGGGGKMRVERQEDFGPALEAAREAESAFDGSVLLERYLT 204
QY 273 QARHLEVOLLADQYNAISIFGRDCSVQRHOKIIEEAPVTIAPEDARESMKAAVRLAK 332
Db 205 KPRHIEMQVFGDRHGNIVHLFERDCSLQRHOKVIEEAPAGMTAEVRAMGDAAVRAAQ 264
QY 333 LVGYVSAGTVEWLYSPSGE-----EFAFLNPRLOVEHPTTEMVSGVNI PAAQLQVANGI 388
Db 265 ALGYVAGATVEFIADVTNGLWPDHDFYFEMNTRLOVEHPTTEITGIDLVEQLRVASGE 324
QY 389 PLYSIRDITLYGMDPRGNEVIDDFSSPESFKTKQKPOQPOGHVACRITAENPDPTGFKP 448
Db 325 PL-----P-----KKQADISMNGWAFEARLYAEDPARGFPL 355
QY 449 GMGALTELNFRSSTWGVSTGSGALHEYADSGFHIFAYGADRSEARKQWVLSL 508

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Db 356 ATGRLTSLFEGISRDV-SGVRQDITPTPYDPLIAKLIIVHGQNRSAALGRLODALKEC 414
Qy 509 SIRGDFRTTVEYLKLTDAFESNKITGWLGLIODLTAERPPADLAV 559
Db 415 RIGGTV-TNRDFLIRLTTEHDFRSCHPDTGLIDREI-ERLTAPVAPGDEAL 463

RESULT 35
B64566
A:Species: Helicobacter pylori (strain 26695)
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64566
R: Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A: Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A: Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A: Reference number: A64566; PMID: 97394467; PMID: 9252185
A: Accession: B64566
A: Molecule type: DNA
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Cross-references: UNIPROT: O25134; UNIPARC: UPI00000D3173; GB: AE000553; GB: AE000511; NID
F: 18-458/Domain: biotin carboxylase homology <BCH>

Query Match 22.8%; Score 662; DB 2; Length 458;
Best Local Similarity 32.1%; Pred. No. 2.2e-39;
Matches 165; Conservative 86; Mismatches 179; Indels 84; Gaps 11;

Qy 38 ITKVLICNGIAA VKEIRSKWAYETFGDERAIEFTVMATPEDLKNADYIRWADQYVE 97
Db 16 LSRILIANRGEIALR AOTIQEMKES-----IAIYSTADKDAHLYNTASAKVC 64

Qy 98 VPGSGNNNNYANVDLIVDAERAGVHVWAGWGHASENPRLPESLAASKHIIFFGPGS 157
Db 65 IGGAKSESILNIPAIISAALFEADAIFFGFLSENQNFVE-ICSHSLSEIFGFSK 122

Qy 158 AMSRIGDKISSTIVAHADVPCMPWSGTGKETWMSDQGLTVSDVYQQAQIHTABEGL 217
Db 123 VMALMSDKSKAKSKVMKEAGHPVIEGSDGLKS-----YQEA-----E 159

Qy 218 EKAEGIPYVMKASBEGGGKIRKCTNGEFGKOLYNA-----VLGEVPGSPFVFMKLAGQ 273
Db 160 EIADKIGYPVITKAAAGGGGRGMRVGDGSKLKNLYLAATEALSAFGDGSVYLEKFPNK 219

Qy 274 ARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEAPVTIAPEDARESMKAAVRLAKL 333
Db 220 PKHIEVQLADKHGNVTHVGERDCSVORRQKLIETTPAVVLEEGVRERLLETAIKAAKY 279

Qy 334 VGYVSAGTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIPTAAQLQVAMGIPLYSI 393
Db 280 IGYVAGCTPFELDSNMKDFYFEMNTLQVEHTISEMVSGLNLNIEWKIAQEKL--- 336

Qy 394 RDITRLYGMDFRGNEVIDFDPSSPESFQTKRQKPOQGHVACRITAENPDTGFKPGMGAL 453
Db 337 -----PKQESFSL-----KGHAIECRITAEADPKK-FYPSPGKI 368

Qy 454 TE-----LNRSTSTWGVSVGTSGALHEYADSQFGHIFAYGADRSEARKQWISLKE 507
Db 369 TEWIAPGGVNRVLD SHAHANYVPT-----HYDSMTGKLVGNGENERAIAKMKRALKE 422

Qy 508 LSTRGDFRTTVEYLKLTDAFESNKITGWLGL 541
Db 423 FKVEG-IKTTIPFHEMLENADFQAKIHTKYLE 455

RESULT 36
AB3352
A: Species: Brucella melitensis (strain 16M)
C: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C: Accession: AB3352
R: Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi-
Nucleic Acids Res. 28, 4317-4331, 2000
A: Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an
A: Reference number: AB3352; PMID: 11058132
A: Accession: AB3352
A: Status: preliminary
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C: Species: Brucella melitensis
C: Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
C: Accession: AB3352
R: DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova
; Mazur, M.; Goltzman, E.; Seikov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete;
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A: Title: The genome sequence of the facultative intracellular pathogen Brucella melite;
A: Reference number: AD3252; PMID: 11756688
A: Accession: AB3352
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-667 <KUR>
A: Cross-references: UNIPROT: Q9VHJ8; UNIPARC: UPI0000057E0A; GB: AE008917; PIDN: AAL51981.
A: Experimental source: strain 16M
C: Genetics:
A: Gene: BMEI0800
A: Map position: I
C: Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C: Keywords: ligase

Query Match 22.7%; Score 660.5; DB 2; Length 667;
Best Local Similarity 32.2%; Pred. No. 5e-39;
Matches 168; Conservative 85; Mismatches 177; Indels 91; Gaps 12;

Qy 37 VITKVLICNGIAA VKEIRSKWAYETFGDERAIEFTVMATPEDLKNADYIRWADQYV 96
Db 1 MIKILIANRGEIACRVIKSAKKGIAT-----VAVYSDADRNALHVMADAEAV 49

Qy 97 EYVPGSGNNNNYANVDLIVDAERAGVHVWAGWGHASENPRLPESLAASKHIIFFGPGG 156
Db 50 HIGPAPSNQSYIVIDKILAAIKGADAVHPGFGFLSENPRFAEALKAA--NVTFIGPPV 107

Qy 157 SAMRSLGDKISSTIVAHADVPCMPWSGTGKETWMSDQGLTVSDVYQQAQIHTABEG 216
Db 108 NAIDAMGDKITTSKLAARAGVSTVP-----GHMGLIED-----ADEA 144

Qy 217 LEKAEKIGYPVMTKASBEGGGKIRKCTNGEFGKOLYNAVILGVPVPS-----PVFVMKLAG 272
Db 145 VRIAGSIGYPVMTKASBEGGGKIRKCTNGEFGKOLYNAVILGVPVPS-----PVFVMKLAG 204

Qy 273 QARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEAPVTIAPEDARESMKAAVRLAK 332
Db 205 QPHIEIQLVQDQHGNNVVLGERECISIQRRNQKIVIEAPSPFLDEATRKMGQAVALAK 264

Qy 333 LVGYVSAGTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIPTAAQLQVAMGIPLY 391
Db 265 AVGYVSAGTVEFTVD--GNRNFYFLEMNTRLQVEHPVTELTITGDLVEEMIRVASGEKILRF 323

Qy 392 SIRDITRLYGMDFRGNEVIDFDPSSPESFQTKRQKPOQGHVACRITAENPDTGFKPGMG 451
Db 324 AQADVKL-----NGWAIESRLYAEADPYRNFLPSIG 353

Qy 452 ALTELN-----FRSSTSTWGVSVGTSGALHEYADSQFGHIFAYGADRSEARK 499
Db 354 RLTRYPYRVEGRNPDCGTVIRNDI---GVPE---GGEISMYDPMIAKLTGWPDRISAID 407

Qy 500 QMWISLKEISIRGDFRTTVEYLKLTDAFESNKITGWL 540
Db 408 AMGHALDAFEVEG-IGHNLPFLSAVMDHPRFRREGALTTAFI 447

RESULT 37
CB3998
A: Species: Brucella melitensis
C: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C: Accession: CB3998
R: Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi-
Nucleic Acids Res. 28, 4317-4331, 2000
A: Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an
A: Reference number: AB3352; PMID: 11058132
A: Accession: CB3998
A: Status: preliminary
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QY 157 SAMRSLGDKLSSITVAQHADVPCMPWSGTGKTMMSDQGLFTVSDVYQACIHTAEAG 216
Db 108 GATEAMGDKITSKLAAGVSTVP-----GHMGLIED-----ADEA 144
QY 217 LEKAEKIGYPMIKASGGGGKGIKCTNGEEFKOLYNALVGEVPGS----PVFVVKLAG 272
Db 145 VKIASQIGYPMIKASAGGGKGMRIAFNEAEAREGFQSSKNEAKSFGDDRIEFIEKFTV 204
QY 273 QARHLEVQLLADQYGNASIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAARLAK 332
Db 205 QPRHIEIQLVGDHGTILYGERECISIQREKQVIEEAPSPFLDEATRHAMGEQAVALAR 264
QY 333 LVGYVSAGTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYS 392
Db 265 AVGYHSAGTVEFVVDGER-NFYFLEMTLQVEHPVTELVTGIDLVEQMIRVASGEKL-- 321
QY 393 IRDITLYGMDPRGNEVIDFDFSSPESFKTORPQGHVHVACRTAENPDTCFKPGMGA 452
Db 322 ----SLAQGDVKLN-----GWAIESRLYAEADPYRNFPSIGR 354
QY 453 LTELN-----FRSSTTWGYFSGTSGALHEYADSFQGHIFAYGADRSEARKQ 500
Db 355 LTRYPPGEGAQDSGTVIRNDT---GVFE---GGEISMYDPMIAKLCGSKGKRETAIDA 408
QY 501 MVISLKELSIKRGDFRTTVEYLIKLETDAPESNKITTTGWL-----DGLIQDRLTAER 552
Db 409 MGEALDRFEVEG-IGHNLPFLSAVMQHERFRSGRLTTGFTIAEEFPEGFGSIEPDETAARK 467
QY 553 PPADLAV 559
Db 468 LSAIAAI 474

RESULT 40
AC2997
hypothetical protein pccA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 31-Dec-2004
R;Accession: AC2997
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
Kage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,
P.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2997
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-677 <KUR>
A;Cross-references: UNIPROT:Q8U924; UNIPARC:UPI00000D2267; GB:AB008689; PIDN:AAL44393.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: pccA
A;Map position: linear chromosome
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
Query Match 22.6%; Score 656.5; DB 2; Length 677;
Best Local Similarity 31.1%; Pred. No. 9.8e-39;
Matches 170; Conservative 95; Mismatches 185; Indels 97; Gaps 13;
QY 37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMDQYV 96
Db 11 MIKKILIANRGEIACRVIKAKMGAT-----VAVYSDADANALHVKMADEAV 59
QY 97 EVFGGNNNNYANVLIVDAERAGVAVWAGHGHASENPRLPESLAASKHILFIIPGPG 156
Db 60 HIGAPFPSSQSYIVIDKLEAIQKTGADAVHPGYGLSENAFAQAL--EKAGVVFVIGPPV 117
QY 157 SAMRSLGDKLSSITVAQHADVPCMPWSGTGKTMMSDQGLFTVSDVYQACIHTAEAG 216
Db 118 GATEAMGDKITSKLAAGVSTVP-----GHMGLIED-----ADEA 154
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QY 217 LEKAEKIGYPMIKASGGGGKGIKCTNGEEFKOLYNALVGEVPGS----PVFVVKLAG 272
Db 155 VKIASQIGYPMIKASAGGGKGMRIAFNEAEAREGFQSSKNEAKSFGDDRIEFIEKFTV 214
QY 273 QARHLEVQLLADQYGNASIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAARLAK 332
Db 215 QPRHIEIQLVGDHGTILYGERECISIQREKQVIEEAPSPFLDEATRHAMGEQAVALAR 274
QY 333 LVGYVSAGTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYS 392
Db 275 AVGYHSAGTVEFVVDGER-NFYFLEMTLQVEHPVTELVTGIDLVEQMIRVASGEKL-- 331
QY 393 IRDITLYGMDPRGNEVIDFDFSSPESFKTORPQGHVHVACRTAENPDTCFKPGMGA 452
Db 332 ----SLAQGDVKLN-----GWAIESRLYAEADPYRNFPSIGR 364
QY 453 LTELN-----FRSSTTWGYFSGTSGALHEYADSFQGHIFAYGADRSEARKQ 500
Db 365 LTRYPPGEGAQDSGTVIRNDT---GVFE---GGEISMYDPMIAKLCGSKGKRETAIDA 418
QY 501 MVISLKELSIKRGDFRTTVEYLIKLETDAPESNKITTTGWL-----DGLIQDRLTAER 552
Db 419 MGEALDRFEVEG-IGHNLPFLSAVMQHERFRSGRLTTGFTIAEEFPEGFGSIEPDETAARK 477
QY 553 PPADLAV 559
Db 478 LSAIAAI 484
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Job time : 50 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:13:07 ; Search time 50 Seconds
(without alignments)
924.314 Million cell updates/sec

Title: US-10-633-835-2
Perfect score: 2907
Sequence: 1 PPDHKAQVQFIGNPLETA.....LDGLQDLTAERPPADLAV 559

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRU COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061.5	70.9	2270	2 US-09-581-909-3	Sequence 3, Appli
2	2060	70.9	802	2 US-09-433-043B-120	Sequence 120, App
3	2060	70.9	2237	1 US-08-354-973-1	Sequence 1, Appli
4	1780	61.2	853	2 US-09-433-043B-119	Sequence 119, App
5	1765.5	60.7	852	2 US-09-433-043B-118	Sequence 118, App
6	1578	54.3	2254	1 US-08-677-010-3	Sequence 3, Appli
7	1578	54.3	2254	1 US-08-790-519-3	Sequence 3, Appli
8	1577.5	54.3	2257	2 US-09-839-477-8	Sequence 8, Appli
9	1569.5	54.0	442	2 US-09-248-796A-17027	Sequence 17027, A
10	1565	53.8	2257	1 US-08-611-107-10	Sequence 10, Appl
11	1565	53.8	2257	1 US-08-422-560A-10	Sequence 10, Appl
12	1565	53.8	2257	2 US-08-468-793-10	Sequence 10, Appl
13	1547.5	53.2	2311	2 US-08-934-386-9	Sequence 9, Appli
14	1543.5	53.1	2325	2 US-08-417-089-6	Sequence 6, Appli
15	1543.5	53.1	2325	2 US-08-695-651-6	Sequence 6, Appli
16	1543.5	53.1	2325	2 US-08-930-285-6	Sequence 6, Appli
17	1543.5	53.1	2325	2 US-08-695-421-6	Sequence 6, Appli
18	1543.5	53.1	2325	2 US-08-697-826A-10	Sequence 10, Appl
19	1502.5	51.7	2089	1 US-08-418-893D-23	Sequence 23, Appl
20	1502.5	51.7	2089	1 US-08-418-893D-24	Sequence 24, Appl
21	1495	51.4	2172	1 US-08-611-107-31	Sequence 31, Appl
22	1417	48.7	489	2 US-09-631-594-74	Sequence 74, Appl
23	1265.5	43.5	506	2 US-09-631-594-76	Sequence 76, Appl
24	1152	39.6	2016	2 US-09-475-252-2	Sequence 2, Appli
25	963.5	33.1	491	1 US-07-956-700B-109	Sequence 109, App
26	963.5	33.1	491	1 US-08-476-537-109	Sequence 109, App
27	963.5	33.1	491	1 US-08-485-607-109	Sequence 109, App

28	963.5	33.1	491	1 US-08-475-879-109	Sequence 109, App
29	963.5	33.1	491	2 US-09-433-043B-109	Sequence 109, App
30	961.5	33.1	491	2 US-09-433-043B-117	Sequence 117, App
31	709.5	24.4	447	1 US-08-611-107-6	Sequence 6, Appli
32	709.5	24.4	447	1 US-08-422-560A-6	Sequence 6, Appli
33	709.5	24.4	447	2 US-08-468-793-6	Sequence 122, App
34	709.5	24.4	593	2 US-09-433-043B-122	Sequence 8, Appli
35	681.5	23.4	453	1 US-08-611-107-8	Sequence 8, Appli
36	681.5	23.4	453	1 US-08-422-560A-8	Sequence 8, Appli
37	681.5	23.4	453	2 US-08-468-793-8	Sequence 6, Appli
38	679.5	23.4	453	1 US-07-956-700B-6	Sequence 6, Appli
39	679.5	23.4	453	1 US-08-476-537-6	Sequence 6, Appli
40	679.5	23.4	453	1 US-08-485-607-6	Sequence 6, Appli
41	679.5	23.4	453	1 US-08-475-879-6	Sequence 6, Appli
42	679.5	23.4	453	2 US-09-433-043B-6	Sequence 121, App
43	679.5	23.4	453	2 US-09-433-043B-121	Sequence 6725, Ap
44	667	22.9	670	2 US-09-328-352-6725	Sequence 17494, A
45	663	22.8	1085	2 US-09-248-796A-17494	

ALIGNMENTS

RESULT 1
US-09-581-909-3
; Sequence 3, Application US/09581909
; Patent No. 6586048
; GENERAL INFORMATION:
; APPLICANT: Graham Keith DIXON
; APPLICANT: John Leslie THAIN
; APPLICANT: John Philip VINCENT
; APPLICANT: No. 6566048bert Friedemann SCHNELL
; APPLICANT: Suberna Jini CHAVDA
; TITLE OF INVENTION: Acetyl-CoA-Carboxylase from Candida Albicans
; FILE REFERENCE: 009901/0270671 - PJF/PHM70303/UST
; CURRENT APPLICATION NUMBER: US/09/581,909
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03857
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: GB 9728897.3
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 3
; LENGTH: 2270
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-581-909-3

Query Match	70.9%;	Score 2061.5;	DB 2;	Length 2270;
Best Local Similarity	70.7%;	Pred No. 28-179;		
Matches 390;	Conservative 63;	Mismatches 98;	Indels 1;	Gaps 1;
QY	9	SOFIGNPLETAPASPVADPIRQKQSHSVITKVLICNNGIAAATKRSIRKWAYETFGDE	68	
DB	70	SHFLGSLVNAEPPSKVRDFVRAHQHTVTSKILLANNGIAAATKRSIRKWAYETFGDE	129	
QY	69	RAIETVTATPDLKVNADYIRMAQYVEVPGSNNNYNDLIYDVAERAGVHAWAG	128	
DB	130	KAIQFTVTATPDLKVNADYIRMAQYVEVPGSNNNYNDLIYDVAERAGVHAWAG	189	
QY	129	WGHASNPRLPSLAASKHIIIFIPPGSAMSLGDKISSTIVAOHADYPCMPWSGTGK	188	
DB	190	WGHASNPRLPSLAASKHIIIFIPPGSAMSLGDKISSTIVAOHADYPCMPWSGTGVD	249	
QY	189	ETWMSDQ-CFLTVDVVOQACIHTAEGLKAEKIGYPMVKASGGGKGRKKTNGE	247	
DB	250	EVKIDPQTNLVSADDIYAKGCTSPEDGLEKAKKIFPPVMIKASGGGKGRKRVDEK	309	
QY	248	EFKQLYNVLGEVPGSPVFMKLAGARHLEVLQDLADYGNALISIFGRDCSVORRHOKII	307	
DB	310	NEITLYNQAANIPGSPIFIMKLAGARHLEVLQDLADYGNALISIFGRDCSVORRHOKII	369	
QY	308	EEAPVTIAPEDARESMEKAARLKLGVVSVAGTVEWLYSPESGEFAFLNRLQVEHP	367	

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Db 370..EAPVTIARKETHEMENAAVRLKLVGYVSAGTVEVLYSHAEKDFYLELNPELVQHP 429
Qy 368 TTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSPSPESFKQKPQ 427
Db 430 TTEMVTGNLPAALQIANGIPMERIRDIRTYGADPHITTDIDFEKSETSLVSQRPT 489
Qy 428 POGHVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYADSQGHI 487
Db 490 PKGCTACRITSEBPGEFKSGSLHLELNFSSNVWGYFSGVNGQSIHSPDSQGHI 549
Qy 488 PAYGADRSEARKQWISLKLSEIRGDFRTTVEYLKLETDAPFNSKITTGWLDGLQIDR 547
Db 550 FAFGENQASRKMVMVALKELSIKELSGRDFRTTVEYLKLETDAPFNSKITTGWLDLITKK 609
Qy 548 LTAERPPADLAV 559
Db 610 LTAERPPDIVAV 621

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RESULT 2

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US-09-433-043B-120
; Sequence 120, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: CORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433.043B
; PRIOR FILING DATE: 1999-10-25
; PRIOR FILING DATE: 1995-06-07
; PRIOR FILING DATE: 1995-06-07
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 120
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-120

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Query Match 70.9%; Score 2060; DB 2; Length 802;
Best Local Similarity 69.1%; Pred. No. 5.4e-180;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

Qy 3 PDHKAVSQFIGNPLETAPSPVADPFRKQGGHSHVITKVLICNNGIAAIVKEIRSIRKWAY 62
Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSIRKWAY 83
Qy 63 ETFGDERAIEFTVMATPEDLVKADYIRMAQYVEVPGGNNNNYANVDLIVDAERAGV 122
Db 84 ETFGDDRTVQVFMATPEDLEANAIEYIRMAQYIEVPGGNNNNYANVDLIVDAERADV 143
Qy 123 HAVWAGHGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182
Db 144 DAVWAGHGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCIPW 203
Qy 183 SGTGKETMDSQ--GFTVSDVDVYQACHTAEBGLEKARKIGYPMWIKASEGGGKGKI 240
Db 204 SGTGV-DTVHVDKTEGLVSDVDIYQKCCCTSPEDGLQAKRIGFPPWIKASEGGGKGKI 262
Qy 241 RKCTNGEEFKOLYNAVLEVPSPVFMVKLAGAARHLEVQLLAQYGNATISIFGRDCSVQ 300
Db 263 QOVEREDFIYALYQQAANEIPGSPFIIMKLGRARHLEVQLLAQYGNATISIFGRDCSVQ 322
Qy 301 RRHQKIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEVLYSPESGEFAFLEINP 360
Db 323 RRHQKIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEVLYSHDDGKFFLEINP 382

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Qy 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSPSPES 420
Db 383 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSPSPES 442
Qy 421 KTQKPOQPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSGTSGALHEYA 480
Db 443 KKQRREPIKPGHCTACRITSEDPNDGFKPGSGTLHELNFSSNVWGYFSGVNGNINHSPS 502
Qy 481 DSQFGHIFAYGADRSEARKQWISLKLSEIRGDFRTTVEYLKLETDAPFNSKITTGWL 540
Db 503 DSQFGHIFAFGENQASRKMVMVALKELSIKELSGRDFRTTVEYLKLETDAPFNSKITTGWL 562
Qy 541 DGLIQDLRTAERPPADLAV 559
Db 563 DDLITHKMTAERPPADLAV 581

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RESULT 3

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US-08-354-973-1
; Sequence 1, Application US/08354973
; Patent No. 5641666
; GENERAL INFORMATION:
; APPLICANT: Vahlensieck, Hans-Friedrich
; APPLICANT: Himmen, Albert
; TITLE OF INVENTION: Fungi Resistant to Soraphen A
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: Patent Dept., 520 White Plains Rd., POB 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,973
; FILING DATE: 13-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: PF/5-19802/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: NO
US-08-354-973-1

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Query Match 70.9%; Score 2060; DB 1; Length 2237;
Best Local Similarity 69.1%; Pred. No. 2.7e-179;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

Qy 3 PDHKAVSQFIGNPLETAPSPVADPFRKQGGHSHVITKVLICNNGIAAIVKEIRSIRKWAY 62
Db 29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSIRKWAY 83
Qy 63 ETFGDERAIEFTVMATPEDLVKADYIRMAQYVEVPGGNNNNYANVDLIVDAERAGV 122
Db 84 ETFGDDRTVQVFMATPEDLEANAIEYIRMAQYIEVPGGNNNNYANVDLIVDAERADV 143
Qy 123 HAVWAGHGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182

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Db 279 LNVQDLYEKGVDVDDGLKAAEEVGYPMIKASEGGGKIRKVNADDFNLFQVQ 338
Qy 258 GEVPGSPFVFMKLAGQARHLEVLQADQYGNASIFGRDCSVQRHOKIIEAPVTIAPE 317
Db 339 AEVPGSPFVFMKLAGQARHLEVLQADQYGNASIFGRDCSVQRHOKIIEAPVTIAPE 398
Qy 318 DARESMKAAVRLAKLVGVYSGAGTVEWLYSPESGEFAFLELNPRLQVEHPPTMVGVNI 377
Db 399 AVPEHMEQCAVKLAKVGVYSGAGTVEWLYS-QDGSFYFLELNPRLQVEHPCTEMVADNL 457
Qy 378 PAQOLQVAMGIPLYSIRDTLYGMDPRGNEVIDFDESSPESFQTKRPOQGHVACRI 437
Db 458 PAQOLQVAMGIPLYSIRDTLYGMDPRGNEVIDFDESSPESFQTKRPOQGHVACRI 510
Qy 438 TAENPDTGFKPGMGALTELNFRSSTTWGYFSVTSGALHEVYADSGFHIIPAYGADRSEA 497
Db 511 TSENPEDEKESPGTQVQLNFRSNKNVWGYFSAAGLHEFADSGFCHCFSGWENREEA 570
Qy 498 RQWVISLKLISIRGDFRTTVEYLKLETAPEFNSKITTGWLDGLQDRLTAERPDL 557
Db 571 ISNMVVALKELSIIRGDFRTTVEYLKLETAPEFNSKITTGWLDGLQDRLTAERPDL 630
Qy 558 AV 559
Db 631 GV 632

RESULT 6
US-08-677-010-3
; Sequence 3, Application US/08677010
; Patent No. 5925805
; GENERAL INFORMATION:
; APPLICANT: Ohlrogge, John B.
; APPLICANT: Roessler, Keith R.
; APPLICANT: Shorrosh, Basil S.
; TITLE OF INVENTION: Structure and Expression of an
; Arabinopsin Acetyl-coenzyme A Carboxylase Gene
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,010
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 6550-00002CPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2254 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-677-010-3

Query Match 54.3%; Score 1578; DB 1; Length 2254;
Best Local Similarity 53.3%; Fred. No. 4.8e-135;

Matches 301; Conservative 97; Mismatches 143; Indels 24; Gaps 5;
Qy 4 DHKAVSQFIGENPLETAPSPVADFIKQGGHGVITKVLICNNNGIAAIVKESIRKWAYE 63
Db 8 NHCNAV-----GPGINVTYQVDFCKALRGKPIHSILIANNGMAAVKESIRVTRWAYE 62
Qy 64 TFGDERAIEFTVMTATPDLKVNADYIRMDQYVEVPGSGNNNNYANVLLIVDVAERAGVH 123
Db 63 TFGTERAIIIVGTMATPDMIRINAEIRIADQFVEVPGTNNNNYANVLLIVDVAERAGVH 122
Qy 124 AVWAGHGHASENPRLPESLAASKHIIIFIGPGSAMRSIGDKISSTTVAOHADVPMPWS 183
Db 123 AVWPGHGHASENPRLPESLAASKHIIIFIGPGSAMRSIGDKISSTTVAOHADVPMPWS 180
Qy 184 GTGKETMMSDQGLVTSDDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKIRK 243
Db 181 GSHVK--IPNSNLVTIPEIYRQACVYTTETEAIASQVVGYPAMIKASWGGGKIRK 238
Qy 244 TNGEERKQLYNALVEVPGSPVFMKLAGQARHLEVLQADQYGNASIFGRDCSVQRH 303
Db 239 HNDDEVRALFKQVQGEVPGSPIFIMKVASQSRHLEVQLLCKHGNVSALHSRDCSVQRH 298
Qy 304 QKIIIEAPVTIAPEDARESMEKAAVRLAKLVGVYSGAGTVEWLYSPESGEFAFLELNPRLQ 363
Db 299 QKIIIEGPITVAPETVKKLEQARLAKSVNVTGATIEYLISMDTGEYFLELNPRLQ 358
Qy 364 VEHTTEMVSGVNIAPAAQLQVAMGIPLYSIRDTLYGMDPRGN-----EVIDPDF 414
Db 359 VEHPVTWIAEINLPAAQVAVGMGIPLWQIPEIRRFYGIHGGYDSWRKTSVVAFPDF 418
Qy 415 SSPESFKTKRPOGHVACRITAEENPDTGFKPGMGALTELNFRSSTTWGYFSVTSG 474
Db 419 DKAQSI-----PKGHCVAVRTSEDDPDGFKPTSGRVOELSFKSKPNWYAFSVKSGG 472
Qy 475 ALHEVADSQFHIIPAYGADRSEARKOWISLKELSIIRGDFRTTVEYLKLETAPEFNSK 534
Db 473 GIHEFSDSQFHVAFGESEALAIANVLGLKELSIIRGDFRTTVEYLKLETAPEFNSK 532
Qy 535 ITTGWLDGLQDRLTAERPDLAV 559
Db 533 IHTGWLDGLQDRLTAERPDLAV 557

RESULT 7
US-08-790-519-3
; Sequence 3, Application US/08790519
; Patent No. 5962767
; GENERAL INFORMATION:
; APPLICANT: Ohlrogge, John B.
; APPLICANT: Roessler, Keith R.
; APPLICANT: Shorrosh, Basil S.
; TITLE OF INVENTION: Structure and Expression of an
; Arabinopsin Acetyl-coenzyme A Carboxylase Gene
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,519
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,630
; FILING DATE:


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; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17027

Query Match      54.0%; Score 1569.5; DB 2; Length 442;
Best Local Similarity 70.2%; Pred. No. 2.3e-135;
Matches 295; Conservative 49; Mismatches 75; Indels 1; Gaps 1;

Qy 101 GSNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPESLAASKHIIIFIGPPGSAMR 160
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 14 GTNNNNYANVDLIVEIAESTNAHAWAGWGHASENPLPEKLAASPKKIIIFIGPPGSAMR 73
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 161 SLGDKISSTIVAAHADVPCMPGSGTGIRKTMMSDQ-GFLTYSDDVYQACHTAELEGLEK 219
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 74 SLGDKISSTIVAAHQAVPCIPWSGTVGDEVIDPOTNLVSVADDIYAKGCTSPEDGLEK 133
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 220 AEKIGYPWIKASSEGKGGKIRKCTNGEEFKQLYNAVLEGPVFMKLAGQARHLEV 279
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 134 AKKIGFPWIKASSEGKGGKIRKVDDEKFNITLYNQAAANEIPGSPIFIMKLAGDARHLEV 193
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 280 QLLADQYGNALISIFGRDCSVORRHOKIIEEAPVTIAPEDARESEKAAVRLAKLVGYVSA 339
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 194 QLLADQYGNALISIFGRDCSVORRHOKIIEEAPVTIAPEDARESEKAAVRLAKLVGYVSA 253
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 340 GTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGPIYSLDIRITL 399
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 254 GTVEWLYSHABDKFYFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGPIYSLDIRITL 313
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 400 YGMDPRGNEVDIFSSPESFKTKORQPOGHVWACRITAENPDTGPKPGMGALTELNFR 459
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 314 YGADPHITTDIDFEKSTSLVSQRPTPKGHCTACRITSDPGEGFKPSGGSHELNFR 373
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 460 SSTTWGVSFGTSGALHEYADSGFHIFAYGADREARKOMVLSKELSGRDFRTTVE 519
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 374 SSSNVWGYFSGNOSHSIFSDSFGHIFAFGENRQASRKHMVALKELSGRDFRTTVD 433
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-08-611-107-10
; Sequence 10, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611.107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-611-107-10

Query Match      53.8%; Score 1565; DB 1; Length 2257;
Best Local Similarity 54.6%; Pred. No. 7.5e-134;
Matches 300; Conservative 91; Mismatches 132; Indels 26; Gaps 5;

Qy 23 SPVADIRKQGHSHVTKULICNGGIAAUKBIRSIKWAYETFGDERAIEFTVMATPEDL 82
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 83 KVNADYIRWADQVVEYVPGSSNNNNYANVDLIVDAERAGVHAWAGWGHASENPRLPESL 142
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 72 RINAERHRIADQFLEVPGGTNNNNYANVDLIVDAERAGVHAWAGWGHASENPELDPAL 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 143 AASKHKIIFITGPPGSAMRSLGDKISSTIVAAHADVPCMPGSGTGIRK---ETMMSDQGLT 199
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 132 --MEKGIIFLGPSSAANGALGDKIGSLIAQAAGVPTLPWSSGHVVKVQETCHS----- 183
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 200 VSDVTVQACIHTAEGLKAEKIGYPMIKASGEGGKIRKCTNGEERFKQLYNVLEGE 259
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 184 IPEIYKNAACVSTTDEAVASCQVVGYPAMIKASGEGGKIRKVNHDDEVRLAFKQVQGE 243
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 260 VPSPVFMVVKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHOKIIEEAPVTIAPEDA 319
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 244 VPSPVFMVVKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHOKIIEEAPVTIAPET 303
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 320 RESMEKAAVRLAKLVGYVSAAGTVEWLYSPESGEFAFLNPRLOVEHPTTEMVSGVNIIP 379
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 304 IKELEQAARLAKCVYQGAATVEWLYSMETGEVYFLELNPRLQVEHPTVEWIAEINLPA 363
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 380 AQLQVAMGPIYSLDIRITLYGMDPRGN-----EVIDDFSSPESFKTKORQPOG 430
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 364 SQVWVGNGIPLYNIPERRFYIEHGGGVHAWKEISAVATKFDLDKQAQSVK-----PKG 417
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 431 HVVACRITAENPDTGPKPGMGALTELNFRSSTSTWGYFSGTSGALHEYADSGFHIFAY 490
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 418 HCVAVRTSDDPDDGPKPTSGRVEELNFKSPNVWAYFSVKSGALHEFSDSQGHVFAF 477
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 491 GADRSEARKOMVLSKELSGRDFRTTVEYLYKLETFDAFESKNKITTGWLDGLIQDLRLTA 550
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 478 GESRSLAIANMVLKKEIQIRGEIRTNVDYTVLLNAAAEYRENNKHTGTWLDSDRIAMVRA 537
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 551 ERPPADLAV 559
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 538 ERPPWYLSV 546
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-422-560A-10
; Sequence 10, Application US/08422560A
; Patent No. 5910626
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; METHODS FOR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
```


; Patent No. 6222099
 ; GENERAL INFORMATION:
 ; APPLICANT: Regents of the University of Minnesota, et al.
 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ACETYL COA CARBOXYLASE GENE
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
 ; STREET: P. O. Box 2938
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/930,285
 ; FILING DATE: 13-APR-1998
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/04625
 ; FILING DATE: 04-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Embretson, Janet E.
 ; REGISTRATION NUMBER: 39,665
 ; REFERENCE/DOCKET NUMBER: 600.318US4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-339-0331
 ; TELEFAX: 612-339-3061
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2325 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal and C-terminal (full length protein)
 ; ORIGINAL SOURCE:
 ; US-08-930-285-6

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377  IPAAQLOVANGIPLYSIDRTITLYGMDPRGNEVIDFD-----FSSPESFKTQRKPOQ 429
467  LPAAQVAVGGIPLWQIPETIRFYGMDYGGG-----YDIWRKTAALATPFNFDEVDSQWPK 522
430  GHVVACRITAEINPDGTGPKQMGALTENLFRSSTGTWGVFSVGTSCALHEYADSOFGHIF 489
523  GHCVAVRIITSEDDGFKPTGGKVKELSKFKPNWAYFVSVKSGGIIHEPADSOFGHAF 582
490  YGADRSEARKQMVISLKBLSIRGDFRTTVYLIKLLETDAPESKNITTTGWLDTGLI 549
583  YGLSRPAAITNMSLALKEIQRGHEIHSNVDTVDLLNASDPRENKIHTGWLDTRIAMRV 642
550  AERPPADLAV 559
643  AERPPWYISV 652

RESULT 17
US-08-695-421-6
; Sequence 6, Application US/08695421
; Patent No. 6268550
; GENERAL INFORMATION:
; APPLICANT: Gengenbach, B. G.
; APPLICANT: Somers, D. A.
; APPLICANT: Wyse, D. L.
; APPLICANT: Gronwald, J. W.
; APPLICANT: Egli, M. A.
; APPLICANT: Lutz, S. M.
; TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE
; TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,421
; FILING DATE: 23-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/417089
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: 08/014326
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 07/917462
; FILING DATE: 21-JUL-1992
; APPLICATION NUMBER: 07/538674
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.318US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-373-6900
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-695-421-6

```

```

Query Match      53.1%; Score 1543.5; DB 2; Length 2325;
Best Local Similarity 53.5%; Pred. No. 7.4e-132;
Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;

QY 20 APASPVADFRKOGGSHSVITKVLICNGIAAAVEKIRSIRKWAYETFGDERAIEFTVMTATP 79
DB 114 ASVSKVVEFCALGKGTPIHSILVANNGMAAKFMSVRTWANDTFGEKAIQIUMATP 173
QY 80 EDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASENRLPL 139
DB 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVGMAQKLGSAVWPGWGHASENPELP 233
QY 140 ESLAASKHKIIFGPPGSMESLGDKISSTIVAHADVPCMPWGSCTGK---ETMMSDQG 196
DB 234 DALTA--GIVFLGPPASSMNALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLD--- 289
QY 197 FLTVDVDDVYQACIHTAEGLKAEKIGYPVMIKASGEGGKGIKCTNGEEFKQLYNAY 256
DB 289 --AIPSEMRYKACVTTTEEAASCOVVGYPAMIKASGEGGKGIKRVHNDDEVRALEPKQV 346
QY 257 LGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPVTIAP 316
DB 347 QGEVPGSPVFMRLASQSRHLEVQLLADQYGNVAALHSRDCSVORRHQKIEEAPVTIAP 406
QY 317 EDARESMEKAARLAKLVGYSAGTVEWLYSPESGEFAFLELNPRLQVHEPHTTEMVSGVN 376
DB 407 RETVKALEQAARLAKAVGVYGAATVEYLYSMETGDIYFLELNPRLQVHEPHTTEMVSGVN 466
QY 377 IPAAQLOVAMGIPLYSIRDIRTLXGMDPRGNEVIDFD-----FSSPESFKTQKQPQ 429
DB 467 LPAAQVAVGMGIPLWQIPEIRFRFYGMDYGGG----YIWRKTAALATPFNDEFVDSQWPK 522
QY 430 GHVACRITAENPDTPGPKGMGALTELNFIRSTSTWGYFSGTSGALHEYADSOFGHIFA 489
DB 523 GHCVAVRIITSEDDPDDGFKPTGCKVKESFKSKPNWAYFSVKSGGIEHPADSOFGHIFA 582
QY 490 YGADRSEARKQWISLKLSEIRGDFRTTVEYLYKLLETDAPESNKITITGMLDGLIQRLT 549
DB 583 YGLSRPAATNMSLALKEIQIRGEIHSNVDTVDLLNASDFRENKIHTGMLDTRIAMRVQ 642
QY 550 AERPPADLAV 559
DB 643 AERPPWTISV 652

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RESULT 18

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US-08-697-826A-10
Sequence 10, Application US/08697826A
Patent No. 6414222

```

GENERAL INFORMATION:

```

APPLICANT: Gengenbach, B. G.
APPLICANT: Somers, D. A.
APPLICANT: Egli, M. A.
APPLICANT: Marshall, L. C.
APPLICANT: Wyse, D. L.
APPLICANT: Lutz, S. M.
APPLICANT: Van Dee, K. L.
APPLICANT: Parker, W. B.
TITLE OF INVENTION: GENE COMBINATIONS FOR HERBICIDE
TITLE OF INVENTION: TOLERANCE IN CORN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

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SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,826A
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04625
FILING DATE: 04-APR-1996
APPLICATION NUMBER: 08/679,826
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.370W01
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3263
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-697-826A-10

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```

Query Match      53.1%; Score 1543.5; DB 2; Length 2325;
Best Local Similarity 53.5%; Pred. No. 7.4e-132;
Matches 294; Conservative 94; Mismatches 141; Indels 21; Gaps 5;

QY 20 APASPVADFRKOGGSHSVITKVLICNGIAAAVEKIRSIRKWAYETFGDERAIEFTVMTATP 79
DB 114 ASVSKVVEFCALGKGTPIHSILVANNGMAAKFMSVRTWANDTFGEKAIQIUMATP 173
QY 80 EDLKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASENRLPL 139
DB 174 EDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVGMAQKLGSAVWPGWGHASENPELP 233
QY 140 ESLAASKHKIIFGPPGSMESLGDKISSTIVAHADVPCMPWGSCTGK---ETMMSDQG 196
DB 234 DALTA--GIVFLGPPASSMNALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLD--- 288
QY 197 FLTVDVDDVYQACIHTAEGLKAEKIGYPVMIKASGEGGKGIKCTNGEEFKQLYNAY 256
DB 289 --AIPSEMRYKACVTTTEEAASCOVVGYPAMIKASGEGGKGIKRVHNDDEVRALEPKQV 346
QY 257 LGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPVTIAP 316
DB 347 QGEVPGSPVFMRLASQSRHLEVQLLADQYGNVAALHSRDCSVORRHQKIEEAPVTIAP 406
QY 317 EDARESMEKAARLAKLVGYSAGTVEWLYSPESGEFAFLELNPRLQVHEPHTTEMVSGVN 376
DB 407 RETVKALEQAARLAKAVGVYGAATVEYLYSMETGDIYFLELNPRLQVHEPHTTEMVSGVN 466
QY 377 IPAAQLOVAMGIPLYSIRDIRTLXGMDPRGNEVIDFD-----FSSPESFKTQKQPQ 429
DB 467 LPAAQVAVGMGIPLWQIPEIRFRFYGMDYGGG----YIWRKTAALATPFNDEFVDSQWPK 522
QY 430 GHVACRITAENPDTPGPKGMGALTELNFIRSTSTWGYFSGTSGALHEYADSOFGHIFA 489
DB 523 GHCVAVRIITSEDDPDDGFKPTGCKVKESFKSKPNWAYFSVKSGGIEHPADSOFGHIFA 582
QY 490 YGADRSEARKQWISLKLSEIRGDFRTTVEYLYKLLETDAPESNKITITGMLDGLIQRLT 549
DB 583 YGLSRPAATNMSLALKEIQIRGEIHSNVDTVDLLNASDFRENKIHTGMLDTRIAMRVQ 642
QY 550 AERPPADLAV 559
DB 643 AERPPWTISV 652

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RESULT 19

Query Match 51.7%; Score 1502.5; DB 1; Length 2089;
Best Local Similarity 53.2%; Pred. No. 3.6e-128;
Matches 291; Conservative 95; Mismatches 140; Indels 21; Gaps 6;


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QY 22 ASPVADPFRKOGGSHVITKVLINNGIAAANKVIRKWAYETGDERAIEFTVMATPED 81
Db 81 AKSVEDYVYKSGGRNRVIRKVLIANNGMAATKSILSMQWYMEFGDERAIOFVAMATPED 140
QY 82 LKNVADYIRMAQOVVEPGSGNNNNYANVDLIDVAERAGVHVAWAGHASENPRLPES 141
Db 141 LKNAEFIRLADSFEVPGGKNNYANVDVITRIAEQGVDAVWPGHASENPKLPNA 200
QY 142 LAASKHKIIFGPPGSAMRSIGDKISSTIVAHADVPCMPWSGT-----GIKETMMSDQ 195
Db 201 L--DKLGKIFGTPGPVMSVLGDKIAANILAAQTAKVPSIPWSGSGFGPDDGQPLQADITEE 258
QY 196 GFLTVSDVVOACIHTAEBGLEKAEKIGYP--VMIKASEGGGKIRKCTNGEEFKOLY 253
Db 259 G--TIPMEIFNKGVLTSADAIVIVANKIGWENGIMIKASEGGGKIRFVDNEADLRNAP 316
QY 254 NAVLGEVPGSPVFMKLAGARHLEVLQADQYGNASIFGRDCSVORRHQKIIEEAPVT 313
Db 317 VOVENEVIGSIFILMQLCKNARHIEVQIVGDOHGNVALNGRDCSTORRFQKIFEEGPPS 376
QY 314 IAPEDARESMEKAARLAKLVGYYSAGTVWLYSPESGEFAPLELNPRLOVEHPTTEMVS 373
Db 377 IVPKETHEMELAAQRLTONIGYQAGTVLYNAADNKPFFLELNPRLOVEHPTTEGIT 436
QY 374 GVNTPAQLQVAMGIPLYSIRDIRTYLM--DPRGNEVIDFDFSSPESFKTORPOQGHV 432
Db 437 GANLPATQLQVAMGIPLYNIPDIRLYGREDAYGTDPID-----FLOERYELDSHV 488
QY 433 VACHITAEINPDTPKPGMGALTEINFRSSTWGVSVGTSALHEYADSOFGHIFAYGA 492
Db 489 IAAKITAENPDGPKTSGSIRTERIKFQSTPNVWGVSVGANGGHEFADSOFGHLFAKGP 548
QY 493 DRSEARKQWISLKELSGIRGFRITVEYLIKLETDAPESNKITTWGLDGLIQDLTAER 552
Db 549 NREQARKALVLAKEMEVGRDIRNSVEYLVKLETEAFKKTIDTSLWLDGLIKEKSVKVE 608
QY 553 PPADLAV 559
Db 609 MPSHLVV 615

```

RESULT 21

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US-08-611-107-31
; Sequence 31, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611.107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2172 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-611-107-31

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Query Match 51.4%; Score 1495; DB 1; Length 2172;

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Best Local Similarity 54.8%; Pred. No. 1.9e-127;
Matches 284; Conservative 87; Mismatches 121; Indels 26; Gaps 5;

QY 54 IRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQOVVEPGSGNNNNYANVDLI 113
Db 2 MRSIRWALTEFTGNEKAILLVATPEDLKNAEHRIADQFLVPGGTNNNNYANVQLI 61
QY 114 VDVAERAGVHVAWAGHASENPRLPESLAASKHKIIFGPPGSAMRSIGDKISSTIVAQ 173
Db 62 VETAEIRTSVAVWPGHASENPELPAAL--MEKGIIFLPGPSAAMGALDKIGSSLIQA 119
QY 174 HADVPCMPWSGTGK---ETMMSDQGLTVSDVVOACIHTAEBGLEKAEKIGYPWIK 230
Db 120 AAGVPTLPWSGSHVKVPQETCHS-----IPEEIKYKNACVSTTDEAVASCQVVGYPAMIK 173
QY 231 ASGGGGKGRKCTNGEEFKQLYNVLGEVPGSPVFMKLAGARHLEVLQADQYGNAI 290
Db 174 ASWGGGGKGRKRVHNDDEVRALFKVQGVGSGPFIIMKVASOSRHLLEVQLCDKGNVA 233
QY 291 SIFGRDCSVORRHQKIIEEAPVTIAPEDARESMEKAARLAKLVGYYSAGTVWLYSPES 350
Db 234 ALHSRDCSVORRHQKIIEEGPITVAPETIKLEQAARLAKVCVQGAATVEYLYSMET 293
QY 351 GEFAPLELNPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDIRTYLGMDPGN--- 407
Db 294 GEYFLELNPRLOVEHPTVEWIAEINLPASQVVGMGIPLYNIPETIRRFYIEHGGGYHA 353
QY 408 -----EVIDDFDSSPESFKTORPOQGHVACRITAENPDTPKPGMGALTEINFRSS 461
Db 354 WKEISAVATKFDLDKQSVK-----PKGHCVAVRVTSEDDPDGFKPESGRVEELNPKSK 407
QY 462 TSTWGVSVGTSALHEYADSOFGHIFAYGADSEARKQWISLKELSGIRGFRITVEYL 521
Db 408 PNWVAIFSVKSGGAIHEFSDSQGHVAFGESLSAIANNVLGLKEIQIRGEIRTNVDYT 467
QY 522 IKLETDAPESNKITTWGLDGLIQDLTAERPPADLAV 559
Db 468 VDLNAAEYRENKIHGTWLDLSRIAMVRAERPPWYLSV 505

```

RESULT 22

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US-09-631-594-74
; Sequence 74, Application US/09631594
; Patent No. 6737237
; GENERAL INFORMATION:
; APPLICANT: MCLEOD, RIMA W.
; APPLICANT: ROBERTS, CRAIG W.
; APPLICANT: ROBERTS, FIONA
; APPLICANT: JOHNSON, JENNIFER J.
; APPLICANT: KIRISITS, MICHAEL
; APPLICANT: FERGUSON, DAVID
; APPLICANT: LYONS, RUSSELL

```

```

; APPLICANT: MUI, ERNEST
; APPLICANT: MACK, DOUG
; APPLICANT: SAMUEL, BENJAMIN
; APPLICANT: GORNICKI, PIOTR
; APPLICANT: ZUTHER, ELLEN
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
; FILE REFERENCE: 19338-90966
; CURRENT APPLICATION NUMBER: US/09/631.594
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 74
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
; US-09-631-594-74

Query Match      48.7%; Score 1417; DB 2; Length 489;
Best Local Similarity 55.2%; Pred. No. 2.7e-121;
Matches 277; Conservative 77; Mismatches 134; Indels 14; Gaps 5;

QY 40 KVLICNGGIAAVKEIRSKWAYETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVP 99
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 RVLIANNGMAATKSIKSMQWAYMELGDDKLLEFVVMATPEDMRANPEFIRRAKIVEP 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 100 GGSNNNNYANVDLVDVAERAGVHVAWAGHASENPRLPESLAASKHKKIIFIGPPGSAM 159
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GGNPNNNYANVDLVCITAVEKVDVAVPWGHAASENPNRL--SELGTFIGPSATVM 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 160 RSLGDKISSTIVAGHADVPCMPWSGTGKETMMSDQGLTVSDVYQQACIHTAELEGLEK 219
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 AALGDKIAANILACTAGVPSIPWSGDSLKATLDSTG--AI PRDIPQATVKSVECEKV 175
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 220 AEKIGYPMWKASGGGGKGIKCTNGEEFKQLYNVLGEVPGSPVPMKLAGQARHLEV 279
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 ADRIGYPMWKASGGGGKGIKCTNGEEFKQLYNVLGEVPGSPVPMKLAGQARHLEV 235
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 280 QLLADQVGNALISIFGRDCSVQRHOKIIEA-PVTIAPEDARESMEKAAVRLAKLVGYVS 338
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 QIVGDEGQVALUSGRDCSTQRRPKIFEEAPPTTVVPHTMKEMEKAAQRLTQSLGYG 295
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 339 AGTVEWLYSPESGFAFLELNPRLQVEHPTTEMVSGVNI PAALQVAMGIPLYSIRDRT 398
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 296 AGTVEWLYSPESGFAFLELNPRLQVEHPTTEMVSGVNI PAALQVAMGIPLYSIRDRT 355
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 399 LYGMDCPRGNEVIDPSSPSFKTORPQOGHVACRIITAEINPDGFKPGMGALTELNF 458
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 FFGDRPNAGDRI--DFINEDYLPQIR-----HYLASRVTAENPDEGFKPTSGVRDLRF 407
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 459 RSSTSTWGYSVGTSGALHEVADSOFGHIIPAYGADRSEARKOMVLSIKELSIKSGDRFTTV 518
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 408 QPLENWWGYSVGASGVGHEVADSOFGHIIPATGNKREARKVLGLKRVDDVGEIRTP 467
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 519 EYLKLETDAFESNKITTWGL 540
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 EYLVLLEDKDFIENRDTWSL 489
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 23

```

US-09-631-594-76
; Sequence 76, Application US/09631594
; Patent No. 6737237
; GENERAL INFORMATION:
; APPLICANT: MCLEOD, RIMA W.
; APPLICANT: ROBERTS, CRAIG W.
; APPLICANT: ROBERTS, FIONA
; APPLICANT: JOHNSON, JENNIFER J.
; APPLICANT: KIRISITS, MICHAEL

```

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; APPLICANT: FERGUSON, DAVID
; APPLICANT: LYONS, RUSSELL
; APPLICANT: MUI, ERNEST
; APPLICANT: MACK, DOUG
; APPLICANT: SAMUEL, BENJAMIN
; APPLICANT: GORNICKI, PIOTR
; APPLICANT: ZUTHER, ELLEN
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
; FILE REFERENCE: 19338-90966
; CURRENT APPLICATION NUMBER: US/09/631.594
; CURRENT FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 76
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
; US-09-631-594-76

Query Match      43.5%; Score 1265.5; DB 2; Length 506;
Best Local Similarity 49.5%; Pred. No. 2.3e-107;
Matches 263; Conservative 70; Mismatches 143; Indels 55; Gaps 6;

QY 40 KVLICNGGIAAVKEIRSKWAYETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVP 99
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 RVLIANNGTAARVCIKSMQWAYMELGDDKLLEFVVMATPEDMRANPEFIRRAKIVEP 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 100 GGSNNNNYANVDLVDVAERAGVHVAWAGHASENPRLPESLAASKHKKIIFIGPPGSAM 159
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GGNPNNNYANVDLVCITAVEKVDVAVPWGHAASENPNRLPALQTLKRTKIWIWGPSQAM 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 160 RSLGDKISSTIVAGHADVPCMPWSGT-----GIKETMMSDQ 195
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LALGDKIGSAVIAQSVNVCVPMWSGETRSPKRAADTQPHSKTRRSISPPHFTRESH 176
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 196 GFLTWSDDVYQQACIHT-----AEGLKAEKIGYPMWKASGGGGKGIKCTNGEEFK 250
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 -HLSISVSQVLTCLMTWTFAPLHVLDCAKIGYPMWKASGGGGKGIKCTNGEEFK 235
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 251 QLYNVLGEVPGSPVPMKLAGQARHLEVQLLADQVGNALISIFGRDCSVQRHOKIIEA 310
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 DAYRQVNEVKGSPVPMKLAGQARHLEVQLLADQVGNALISIFGRDCSVQRHOKIIEA 295
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGFAFLELNPRLQVEHPTTE 370
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 296 PVVAAPPEVVSQMEDACRMNAVGVENAGTCEFLYDPKTHQPAFLEVNARLQVEHVTE 355
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 371 MVSGVNI PAALQVAMGIPLYSIRDITLYGMDCPRGNEVIDPSSPSFKTORPQOG 430
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 CVGDFNLPAALQVAMGILIDDIIDDKA-----YLDASAASN-----KPVG 395
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 431 -HVACRIITAEINPDGFKPGMGALTELNFIRSTSTWGYSVGTSGALHEVADSOFGHIPA 489
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 396 KHIIAARITAEHAESFRTVGLVHLELTPRSPRFGVGYSGIKGNIHAFNDAQFGLHA 455
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 490 YGADRSEARKOMVLSIKELSIKSGDRFTTVYLYKLETDAFESNKITTWGL 540
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 456 HGDRREARKVHVLAKMDIIRGELTNVEALIKILEHPDFVNAVETHITWL 506
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 24

```

US-09-475-252-2
; Sequence 2, Application US/09475252
; Patent No. 6514726
; GENERAL INFORMATION:
; APPLICANT: DORT, PATRICK K.
; APPLICANT: PARKINSON, TANYA
; APPLICANT: BULAWA, CHRISTINE ELLEN

```

;; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS ACETYL COENZYME-A CARBOXYLASE GENES
;; FILE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
;; FILE REFERENCE: 06286/107001
;; CURRENT APPLICATION NUMBER: US/09/475,252
;; CURRENT FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US 60/114,580
;; PRIOR FILING DATE: 1998-12-31
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 2016
;; TYPE: PRT
;; ORGANISM: Aspergillus fumigatus
US-09-475-252-2

Query Match 39.6%; Score 1152; DB 2; Length 2016;
Best Local Similarity 75.2%; Pred. No. 5,2e-96;
Matches 221; Conservative 29; Mismatches 44; Indels 0; Gaps 0;
QY 266 FVVKLAGOARHLEVOLLADQVGNISIFGRDCSVORHOKIIEAPVTIAPEDARESMEK 325
DB 2 FIMKLAGOARHLEVOLLADQVGNISIFGRDCSVORHOKIIEAPVTIAPEDARESMEK 61
QY 326 AAVRLAKLVGVSAAGTVEWLYSPESGEFAFLELNPRLOVHEPTTEMVSGVNIIPAAQLQVA 385
DB 62 AAVSLGLKLVGVSAAGTVEWLYSHADDFEFLNPRLOVHEPTTEMVSGVNLPAALQIA 121
QY 386 MGPIYSIRDIRTYLGMDFRNEVIDFDFSSPESFKTORPQGHVACRITAENPDGT 445
DB 122 MGPIHRIIRLYGVDPNTSSIDFDFSSPESFKTORPQGHVACRITAENPDGT 181
QY 446 FKPGMGALTENPRSSSTWGVFSGTSGALHEVADSFQGHIFAYGADRSEARKQWISL 505
DB 182 FKPSSTGMELNPRSSSNVGVFSGTAGGHSFSDSQGHIFAYGADRSEARKQWISL 241
QY 506 KELSIRGDFRTTVEYLKLETFADFESNKITGMLDGLIODRLTAERPPADLAV 559
DB 242 KELSIRGDFRTTVEYLKLETFADFESNKITGMLDGLIODRLTAERPPADLAV 295

RESULT 25
US-07-956-7008-109
; Sequence 109, Application US/079567008
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,7008
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 109:

;; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474
; IDENTIFICATION METHOD: Xaa = any amino acid
; US-07-956-7008-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;
QY 227 VMKASEGGGKIRKCTNGEEFKQLYNALVGEVPGSPVFMKLAGOARHLEVOLLADQY 286
DB 1 VMKASWGGGKIRKVNDDVRLFKQVQGEVPGSPFIMKVASQSRHLEVOLLCDKH 60
QY 287 GNAISIFGRDCSVORHOKIIEAPVTIAPEDARESMEKAARLAKLVGVSAAGTVEWLY 346
DB 61 GNVAAHLSDCSVQRHOKIIEBEGPITVAPPETIKEQAARLAKCVYQGAATVEVLY 120
QY 347 SPESGEFAFLELNPRLOVHEPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDIRTYLGMDFR 406
DB 121 SMETGEYFLELNPRLOVHEPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDIRTYLGMDFR 180
QY 407 N-----EVIDFDFSSPESFKTORPQGHVACRITAENPDGTGFKPGMGALTEN 457
DB 181 GYHAWKEISAVATKFDLKAQSVK-----PKGHCVAVRVTSDDPDDGFKPTSGRVEELN 234
QY 458 FRSSSTWGVFSGTSGALHEVADSFQGHIFAYGADRSEARKQWISLKLSTIRGDFRTT 517
DB 235 FKSPKNVWAYFVYSGGAIHEFSDSQGHVFXAGSRLAIANMVLGLKEIQIRGEIRTN 294
QY 518 VEYLKLETFADFESNKITGMLDGLIODRLTAERPPADLAV 559
DB 295 VDTVDLLNAAEYREXNKIHTGMLDGLIODRLTAERPPADLAV 336

RESULT 26
US-08-476-537-109
; Sequence 109, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474
; IDENTIFICATION METHOD: Xaa = any amino acid
; US-08-476-537-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

QY 227 VMKASGGGKGIKCTNGEEFKQLYNALGVPGSPVFMKLAGQARHLEVOLLADQY 286
Db 1 VMKASGGGKGIKRVHNDDEVRLFKQVQGEVPGSPIFIMKVASQSRHLEVOLLCDKH 60

QY 287 GNAISIFGRDCSVORRHQKIEEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLY 346
Db 61 GNVAAHSDCSVORRHQKIEEGPITVAPPETIKEQAARRLAKVCVQGAATVEYLY 120

QY 347 SPESGEFAFLELNPRLQVEHPTTVMVSGVNIIPAAQLQVAMGIPLYSIDRTLYGMDPRG 406
Db 121 SMETGEYFLELNPRLQVEHPVTWIAEINLPASVVVGMGIPLYNIPETIRFYGIEHGG 180

QY 407 N-----EVIDDFSSPESFKTKRQPOQGHVACRTAENPDTPGKPGMGALTELN 457
Db 181 GYHAWKEISAVATKFDLDKQSVK-----PKGHCVAVRVTSEDDPGFKPTSGRVEELN 234

QY 458 FRSTSTWGYFVSGTSGALHEYADSOFGHIFAYGADRSEARKQMWISLKELSRGDFRTT 517
Db 235 FKSKPNWAFVSVXSGALHEFSDSQFGHVFXAGESRLAIANMVLGLKEIQIRGEIRTN 294

QY 518 VEYLKLETDAPESNKITTGWLDGLIQDLRTAERPPADLAV 559
Db 295 VDYTVDLLNAAEYREXNIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 27
US-08-485-607-109
; Sequence 109, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474
; IDENTIFICATION METHOD: Xaa = any amino acid
; US-08-485-607-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

QY 227 VMKASGGGKGIKCTNGEEFKQLYNALGVPGSPVFMKLAGQARHLEVOLLADQY 286
Db 1 VMKASGGGKGIKRVHNDDEVRLFKQVQGEVPGSPIFIMKVASQSRHLEVOLLCDKH 60

QY 287 GNAISIFGRDCSVORRHQKIEEAPVTIAPEDARESMEKAARLAKLVGYVSAGTVEWLY 346
Db 61 GNVAAHSDCSVORRHQKIEEGPITVAPPETIKEQAARRLAKVCVQGAATVEYLY 120

QY 347 SPESGEFAFLELNPRLQVEHPTTVMVSGVNIIPAAQLQVAMGIPLYSIDRTLYGMDPRG 406
Db 121 SMETGEYFLELNPRLQVEHPVTWIAEINLPASVVVGMGIPLYNIPETIRFYGIEHGG 180

QY 407 N-----EVIDDFSSPESFKTKRQPOQGHVACRTAENPDTPGKPGMGALTELN 457
Db 181 GYHAWKEISAVATKFDLDKQSVK-----PKGHCVAVRVTSEDDPGFKPTSGRVEELN 234

QY 458 FRSTSTWGYFVSGTSGALHEYADSOFGHIFAYGADRSEARKQMWISLKELSRGDFRTT 517
Db 235 FKSKPNWAFVSVXSGALHEFSDSQFGHVFXAGESRLAIANMVLGLKEIQIRGEIRTN 294

QY 518 VEYLKLETDAPESNKITTGWLDGLIQDLRTAERPPADLAV 559
Db 295 VDYTVDLLNAAEYREXNIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 28
US-08-475-879-109
; Sequence 109, Application US/08475879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879

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```
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474
; IDENTIFICATION METHOD: Xaa = any amino acid
US-08-475-879-109

Query Match 33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

Qy 227 VMKASGGGGKIRKCTNGEEFKQLYNALVGEVPGSPFVFMKLAGQARHLEVLQADQY 286
Db 1 VMKASGGGGKIRKVNDDVRALFKQVGEVPGSPFIFMKVASQSRHLEVLQCDKH 60

Qy 287 GNAISIFGRDCSVQRHKKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLY 346
Db 61 GNVAAHLSRDCSVQRHKKIIEEGPITVAPETIKELEQAARRLAKVCVQGAATVEVLY 120

Qy 347 SPESGEPAFLNPLRQVHEPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYCMDPRG 406
Db 121 SMETGEYFFLELNPRLQVHEPVTIEWIAEINLPASQVVVGMIPLYNIPERFFYGIHGG 180

Qy 407 N-----EVIDDFSSPSFKTKRQKPOQGHVACRITAEHPDTGFKPMGALTEN 457
Db 181 GYHAWKEISAVATKFDLKAQSVK-----PKGHCVAVRVTSEDDDDGFKPTSGRVEELN 234

Qy 458 FRSETSTWGYFSVGTSGALHEYADSQGHIFAYGADRSEARKQMVISLKELSIKRGDFETT 517
Db 235 FKSKPNWAYFSVXSGAIHEFSDQGHVFAXGESRSLAIANNMVLGLKEIQIRGEIRTN 294

Qy 518 VEYLKLETDAPESNKITTGWLDGLIQDRLTAERPPADLAV 559
Db 295 VDYTVDLLNAAEYREXNIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 29
US-09-433-043B-109
; Sequence 109, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 109
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-117

Query Match 33.1%; Score 961.5; DB 2; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.8e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15; Gaps 2;

Qy 227 VMKASGGGGKIRKCTNGEEFKQLYNALVGEVPGSPFVFMKLAGQARHLEVLQADQY 286
Db 1 VMKASGGGGKIRKVNDDVRALFKQVGEVPGSPFIFMKVASQSRHLEVLQCDKH 60

Qy 287 GNAISIFGRDCSVQRHKKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLY 346
Db 61 GNVAAHLSRDCSVQRHKKIIEEGPITVAPETIKELEQAARRLAKVCVQGAATVEVLY 120

Qy 347 SPESGEPAFLNPLRQVHEPTTEMVSGVNIPAAQLQVAMGIPLYSIRDITLYCMDPRG 406
Db 121 SMETGEYFFLELNPRLQVHEPVTIEWIAEINLPASQVVVGMIPLYNIPERFFYGIHGG 180

Qy 407 N-----EVIDDFSSPSFKTKRQKPOQGHVACRITAEHPDTGFKPMGALTEN 457
Db 181 GYHAWKEISAVATKFDLKAQSVK-----PKGHCVAVRVTSEDDDDGFKPTSGRVEELN 234

Qy 458 FRSETSTWGYFSVGTSGALHEYADSQGHIFAYGADRSEARKQMVISLKELSIKRGDFETT 517
Db 235 FKSKPNWAYFSVXSGAIHEFSDQGHVFAXGESRSLAIANNMVLGLKEIQIRGEIRTN 294

Qy 518 VEYLKLETDAPESNKITTGWLDGLIQDRLTAERPPADLAV 559
Db 295 VDYTVDLLNAAEYREXNIHTGWLDSRIAMRVRAERPPWYLSV 336

RESULT 30
US-09-433-043B-117
; Sequence 117, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 117
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-117
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QY 287 GNAISIFGRDCSVORRHOXIIIEAPVTIAPEDARESMKAAVRLAKLVGVYUSACTVWLY 346
DB 61 GNAALHSRDCSVORRHOXIIIEEPTVAPPETIKELEQOAAARRLAKCVQYGAATVEYL 120
QY 347 SPESGEFAFLNRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRG 406
DB 121 SMETGEYFLELNLRLQVEHPTVEIAEINLPASQVVGMPILYNIPEIRRFYIEHGG 180
QY 407 N-----EVIDFSSPESFKTORQPOQGHVACRITAENPDGFKPGMGALTELN 457
DB 181 GYHAWKEISAVATFDLDKAWSVK-----PKGHCVAVRVTSEDDGFKPFGTSGRVBEELN 234
QY 458 FRSTSTWGVYFSGVGTSGALHAYDSOFCHIFAYGADRSEARKOMVISIKELSIIRGDFRTT 517
DB 235 FKSPNWAYFSVKSGGAIHFSQSGHGFAPGESRLALANWVLGKELQIRGEIRTN 294
QY 518 VEYLKLETTDAFESNKITTLGWLGLQIDRLTAERPPADLAV 559
DB 295 VDYTVDLLNAAEYRENMHTGMLDSRIAMRVRAERPPWYLSV 336

RESULT 31
US-08-611-107-6
; Sequence 6, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611.107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-611-107-6

Query Match 24.4%; Score 709.5; DB 1; Length 447;

Best Local Similarity 32.9%; Pred. No. 2.le-56;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;
QY 40 KVLICNNGIAA VKBIRSIRKWAYETFGDBRAIEFTYMATPEDLKVNADYIRMDQVYVEVP 99
DB 5 KILIANRGEIALRILRACEEMGIATI-----AVHSTV-----DRNALHVQLADEAVCIG 53
QY 100 GGSNNNNYANVDLIVDAERAGVHAWAGHCHASENPRLPESLAAASHKHIIIFIGPGSAM,159
DB 54 EPASAKSYLNIPNIIAALTRNASAIHPGYGFLUSENAKFAEICA--DHHIAFTIGTPEAI 111
QY 160 RSLGDKISSITVAHADVPICMPMSGTGKIKETMMSDQGLTVDVYQACIHTAESELEK 219
DB 112 RLMGDKSTAKETMQKAGVTVPGS-----EGLVETEQEGLEL 148
QY 220 AEKIGYPMVMIKASEGGGKIRKCTNGEBFKQLYNALVGEV-----PGSPVFMKLAGQAR 275
DB 149 AKDIGYPMVMIKATAGGGRGMLRVSPDEFVKLFLAAQGEAGAAFGNAGVYIEKFIERPR 208
QY 276 HLEVOLLADQYGNALISIFGRDCSVORRHOXIIIEAPVTIAPEDARESMKAAVRLAKLVG 335
DB 209 HIEFOILADNYGNVHILGERDCSIQRNOKLLEAPSPALDSLREKMGQAAVKAQOFIN 268
QY 336 YVSAGTVEWLYSPESGEFAFLNRLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395
DB 269 YTCAGTIEFLLD-RSQGFYFMEWNTRIQVEHPTVEMTVGVLLVEQIRIAQGERLRLTQD 327
QY 396 IRTLYGMDPRGNEVIDDFSSPESFKTORQPOQGHVACRITAENPDGFKPGMGALTE 455
DB 328 QVVV-----RGHAIECRINAEDPDHDFRAPGRIS- 357
QY 456 LNFIRSTSTWGVYFSGVTSGA-----LHEYADSOFGHIFAYCADSEARKOMVIS 504
DB 358 -----GYLPPGGPGVRIDSHVYTDYQIPPYDLSLIGKLVWGPDRATAINRMKRA 407
QY 505 LKELSIIRGDFRTTVEYLKLETTDAFESNKITTLGWL 540
DB 408 LRECAITG-LPTTIGHFQRIMENPQFLQGNVSTSFV 442

RESULT 32
US-08-422-560A-6
; Sequence 6, Application US/08422560A
; Patent No. 5910626
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,560A
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/956,700
; FILING DATE: 02-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:152/WIM


```

US-09-433-043B-122
; Sequence 122, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:38US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR FILING DATE: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR FILING DATE: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 122
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-122

Query Match 24.4%; Score 709.5; DB 2; Length 593;
Best Local Similarity 32.9%; Pred. No. 3.3e-56;
Matches 170; Conservative 88; Mismatches 165; Indels 93; Gaps 10;

Qy 40 KVLICNNGIAA VKETSRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99
Db 5 KILLANRGEIALRIIRACEEINGIAT-----AVHSTV-----DRNALHVQLADEAVCIG 53
Qy 100 GGSNNNNYANDLIVDVAERAGVHVAWAGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGLFSENARFAEICA--DHIIAFIQTPEAI 111
Qy 160 RSLGDKISSTIVAHADVPCMPWSGTGKETMMSDQGLTVSDVYQACHTAEGLK 219
Db 112 RLMGDKSTAKETMQKAGVPTVPGS-----EGLVETEQEGLEL 148
Qy 220 AEKIGYPMIKASGEGGKGRKCTNGEFPKOLYNALVGEV-----PGSPVFMKLAGQAR 275
Db 149 AKDIGYPMIKATAGGGGRGRLVRSDFEVLKFLAAGGAGAAFGNAGVIEFIERPR 208
Qy 276 HLEVQLLADQYGNNAISIFGRDCSVQRHKKIIEEAPVTIAPEDARESMKAAVRLAKLVG 335
Db 209 HIEFQILADNYGNVHLGERDCSIQRRNQKLEEPSALOSDLREKMGQAAVKAQAFIN 268
Qy 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPHTTEMVSGVNIIPAAQLQVANGIPLYSIRD 395
Db 269 YAGAGTIEFLLD-RSGQFYFEMNTRIQVEHPVTEMTIQTGVDLLVEQIRIAQGERLRLTQD 327
Qy 396 IRTLYGMDPRGNEVIDDFSSPESFKTORQKPOQGHVVACRITAENPDTPGKPGMGALTE 455
Db 328 QVVL-----RGHAIECRINAEDPDHDFRPAGRIS- 357
Qy 456 LNFRSSTWGYFVSGTSGA-----LHEYADSQFGHIIFAYGADRSEARKQMVIS 504
Db 358 -----CYLPPGGPGVRIDSHVYTDYQIPPYDSLICKLIVMGDPDRATAINRMKRA 407
Qy 505 LKELISRGDFTTVEYLKILETDAFESNKITGWL 540
Db 408 LRECAITG-LPTTIGFHFHORMENPQFLQGNVSTSFV 442

RESULT 35
US-08-611-107-8
; Sequence 8, Application US/086111107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr

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; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-611-107-8

Query Match 23.4%; Score 681.5; DB 1; Length 453;
Best Local Similarity 32.1%; Pred. No. 8e-54;
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

Qy 40 KVLICNNGIAA VKETSRKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYVEVP 99
Db 5 KILLANRGEIALRIIRACEEINGIAT-----AVHSTV-----DRNALHVQLADEAVCIG 53
Qy 100 GGSNNNNYANDLIVDVAERAGVHVAWAGHASENPRLPESLAASKHKIIFIGPPGSAM 159
Db 54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGLFSENARFAEICA--DHIIAFIQTPEAI 111
Qy 160 RSLGDKISSTIVAHADVPCMPWSGTGKETMMSDQGLTVSDVYQACHTAEGLK 219
Db 112 RLMGDKSTAKETMQKAGVPTVPGS-----EGLVETEQEGLEL 148
Qy 220 AEKIGYPMIKASGEGGKGRKCTNGEFPKOLYNALVGEV-----PGSPVFMKLAGQAR 275
Db 149 AKDIGYPMIKATAGGGGRGRLVRSDFEVLKFLAAGGAGAAFGNAGVIEFIERPR 208
Qy 276 HLEVQLLADQYGNNAISIFGRDCSVQRHKKIIEEAPVTIAPEDARESMKAAVRLAKLVG 335
Db 209 HIEFQILADNYGNVHLGERDCSIQRRNQKLEEPSALOSDLREKMGQAAVKAQAFIN 268
Qy 336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPHTTEMVSGVNIIPAAQLQVANGIPLYSIRD 395
Db 269 YAGAGTIEFLLD-RSGQFYFEMNTRIQVEHPVTEMTIQTGVDLLVEQIRIAQGERLRLTQD 327
Qy 396 IRTLYGMDPRGNEVIDDFSSPESFKTORQKPOQGHVVACRITAENPDTPGKPGMGALTE 455

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Db 320 -----EALRF-----ROADQLRGHAEICRINAEDEYNFRPNPGRIT- 357
Qy 456 LNRFSSTWGYFSGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 358 -----GYLPPGGVGRVDSHVYTDYEIPPYDSLICKLIVMGATREAIARMORA 407
Qy 505 LKELSIRGDFRTTVEYLKLETDAPESNKITTTGWLGLIQRDL 548
Db 408 LRECAITG-LPTTILSFHQLMQLMPEFLRGELYTNFVEQVMLPRI 450

RESULT 36
US-08-422-560A-8
; Sequence 8, Application US/08422560A
; Patent No. 5910626
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; METHODS FOR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,560A
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/956,700
; FILING DATE: 02-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:152/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-422-560A-8

Query Match 23.4%; Score 681.5; DB 1; Length 453;
Best Local Similarity 32.1%; Pred. No. 8e-54;
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

Qy 40 KVLICNNGIAVKEIRSKWAYETFGDERAIEFTVMATPDLKVNADYIRMAQYVEVP 99
Db 5 KILIANRGEIALRLTCEELGIGTI-----AVHSTV-----DRNALHVLQADEAVCIG 53
Qy 100 GGSNNNNYVDLVDVAERAGVAVAGWAGHASENPRLPESLASKHKIIFGPPGSAM 159
Db 54 EAASKSVLNPINPIAALTRNASAIHFGYFLAENARFAICA--DHHLTFIGSPDSI 111
Qy 160 RSLGDKISSTTVAQHADYPCWPWSGTGKGTMTMSDQGLTVDYVQOACHTTAEGLK 219
Db 112 RAMGDKSTAKETMRVGVPTIPGS-----DGLLT--DV-----DSAAKV 148
Qy 220 AEKIGYPMVIMKASEGGGKGIRKCTNGEEFKQLYNVLGEVP-----GSP-VTFMKLAGOAR 275

Db 149 AAEIGPVMKATAGGGGRGNRLVRPADLEKFLAAQGEAREAFNGPGHYLEKFIORPR 208
Qy 276 HLEVQLLADQYGNNAISIFGRDCSVQRHQRKIIEAPVTIAPEDARESMKAAVRLAKLVG 335
Db 209 HVEFQILADAYGNVHLGRDCSIQRHQRKLEAPSPALSDLRQKMGDAAVKVAQIG 268
Qy 336 YVSAGTVEMLYSPESGEFAPLELNPRLQVHEPPTMVGWVNIIPAAQLQVAMGIPLYSIRD 395
Db 269 YIGAGTVEFLVD-ATGNFYFMENMTRIQVEHPVTEMITGLDLIABQIRIAQG----- 319
Qy 396 IRTLYGMDPRGNEVIDFSSPESFKTQRKQPOGHVACRITAEENPDCTKPGMGALTE 455
Db 320 -----EALRF-----ROADQLRGHAEICRINAEDEYNFRPNPGRIT- 357
Qy 456 LNRFSSTWGYFSGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS 504
Db 358 -----GYLPPGGVGRVDSHVYTDYEIPPYDSLICKLIVMGATREAIARMORA 407
Qy 505 LKELSIRGDFRTTVEYLKLETDAPESNKITTTGWLGLIQRDL 548
Db 408 LRECAITG-LPTTILSFHQLMQLMPEFLRGELYTNFVEQVMLPRI 450

RESULT 37
US-08-468-793-8
; Sequence 8, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,793
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,560
; FILING DATE: 14-APR-1995
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; CLASSIFICATION: 800
; APPLICATION NUMBER: PCT/US93/09340
; FILING DATE: 30-SEP-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-6

Query Match 23.4%; Score 679.5; DB 1; Length 453;
Best Local Similarity 32.1%; Pred. No. 1.2e-53;
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

QY 40 KVLICNGIAAVKEIRSKWAYETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVP 99
DB 5 KILIANGETALRLTCEELGIGTI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHIIIFIGPPQSAM 159
DB 54 EAASSKSYLNPINIIAALTRNASAIHPGYGFLAENARFAEICA--DHLLTFIGSPDSI 111

QY 160 RSLGDKLSSITVAQHADVPCMPWMSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLEK 219
DB 112 RAMGDKSTAKETMQRVGVTIPGS-----DGLLT---DV-----DSAAKV 148

QY 220 AEKIGYPMVKASGGGKGIRKCTNGEEFKOLYNVAVLGEVP---GSP-VFVVKLAGOAR 275
DB 149 AAEIGYPMVKATAGGGRGWRLVREPADLEKFLAAQGEAAAFNGPGLYLEKFIIDRPR 208

QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRHOKIIEEAPVTIAPEDARESMEKAAYLAKLVG 335
DB 209 HVBEQILADAYGNVVELGERDCSIORRHOKLLEAPSPALSADLRQKMGDAAVKVAQIG 268

QY 336 YVSAGTVEWLYSPESGEPFALELNPRLOVEHPVTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395
DB 269 YIGAGTVEFLVD-ATGNFYPMENMTRIQVEHPVTTEMITGLDLIAEQIRIAGQ----- 319

QY 396 IRTLYGMDPRGNEVIDDFSSPESFKTKQKPOGHVACRITAENPDTPGKPGMGALTE 455
DB 320 -----EALRP-----ROADIQLRGAIECRINAEDPEYFRPNPGRIT- 357

QY 456 LNFRSSTSTWGYFSGVTSGA-----LHEYADSQFHIFAYGADRSEARKQMVIS 504
DB 358 -----GYLPPGGPGVRVDSHVYTDYEIPPYDLSLICKLVWGTATREEARMORA 407

QY 505 LKELISRGDFRTTVEYLKLETDAPESNKITTTGWLGLIQDRL 548
DB 408 LREGAITG-LPTTILSFHQLMQMPEFLRGELYTNFVEQWMLPRI 450

RESULT 40
US-08-485-607-6
; Sequence 6, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Cornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
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; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk.
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-485-607-6

Query Match 23.4%; Score 679.5; DB 1; Length 453;
Best Local Similarity 32.1%; Pred. No. 1.2e-53;
Matches 168; Conservative 97; Mismatches 166; Indels 93; Gaps 14;

QY 40 KVLICNGIAAVKEIRSKWAYETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVP 99
DB 5 KILIANGETALRLTCEELGIGTI-----AVHSTV-----DRNALHVQLADEAVCIG 53

QY 100 GGSNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHIIIFIGPPQSAM 159
DB 54 EAASSKSYLNPINIIAALTRNASAIHPGYGFLAENARFAEICA--DHLLTFIGSPDSI 111

QY 160 RSLGDKLSSITVAQHADVPCMPWMSGTGIKETMMSDQGLTVSDVYQQACIHTAEGLEK 219
DB 112 RAMGDKSTAKETMQRVGVTIPGS-----DGLLT---DV-----DSAAKV 148

QY 220 AEKIGYPMVKASGGGKGIRKCTNGEEFKOLYNVAVLGEVP---GSP-VFVVKLAGOAR 275
DB 149 AAEIGYPMVKATAGGGRGWRLVREPADLEKFLAAQGEAAAFNGPGLYLEKFIIDRPR 208

QY 276 HLEVQLLADQYGNNAISIFGRDCSVQRHOKIIEEAPVTIAPEDARESMEKAAYLAKLVG 335
DB 209 HVBEQILADAYGNVVELGERDCSIORRHOKLLEAPSPALSADLRQKMGDAAVKVAQIG 268

QY 336 YVSAGTVEWLYSPESGEPFALELNPRLOVEHPVTTEMVSGVNIIPAAQLQVAMGIPLYSIRD 395
DB 269 YIGAGTVEFLVD-ATGNFYPMENMTRIQVEHPVTTEMITGLDLIAEQIRIAGQ----- 319

QY 396 IRTLYGMDPRGNEVIDDFSSPESFKTKQKPOGHVACRITAENPDTPGKPGMGALTE 455
DB 320 -----EALRP-----ROADIQLRGAIECRINAEDPEYFRPNPGRIT- 357

QY 456 LNFRSSTSTWGYFSGVTSGA-----LHEYADSQFHIFAYGADRSEARKQMVIS 504
DB 358 -----GYLPPGGPGVRVDSHVYTDYEIPPYDLSLICKLVWGTATREEARMORA 407

QY 505 LKELISRGDFRTTVEYLKLETDAPESNKITTTGWLGLIQDRL 548
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Db 408 LREGAIG-LPTTISFHOLQMPFELRGELYTNFVEQVMLPRI 450

Search completed: February 4, 2006, 18:14:38
Job time : 55 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:05:17 : Search time 248 Seconds
(without alignments)
1590.284 Million cell updates/sec

Title: US-10-633-835-2

Perfect score: 2907

Sequence: 1 PPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPPADLAV 559

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2907	100.0	2185	Q4P514_USTMA	Q4P514 ustilago ma
2	2896	99.6	2185	Q12721_USTMA	Q12721 ustilago ma
3	2269	78.1	2237	Q5KFC9_CRYNE	Q5KFC9 cryptococcus
4	2269	78.1	2237	Q55Q76_CRYNE	Q55Q76 cryptococcus
5	2190	75.3	2288	Q60033_EMENI	Q60033 emericella
6	2190	75.3	2288	Q5B004_EMENI	Q5B004 aspergillus
7	2186	75.2	2292	Q4X1V2_ASFPF	Q4X1V2 aspergillus
8	2179	75.0	2275	Q7SBL5_NEUCR	Q7SBL5 neurospora
9	2163	74.4	2344	Q5IYC2_MAGGR	Q5IYC2 magnaporthe
10	2148	73.9	2271	Q41878_GIBZE	Q41878 gibberella
11	2100.5	72.3	2231	Q6CL34_KIJULA	Q6CL34 kluyveromyces
12	2090.5	71.9	2233	Q6FKK8_CANGA	Q6FKK8 candida gla
13	2090.5	71.9	2280	COAC_SCHPO	P78820 schizosacch
14	2084	71.7	2266	Q6CC31_YARLI	Q6CC31 yarrowia li
15	2069.5	71.2	2231	Q7SEK8_ASHGO	Q7SEK8 ashbya goss
16	2061.5	70.9	2271	Q5AAM4_CANAL	Q5AAM4 candida alb
17	2060	70.9	2233	COAC_YEAST	Q00955 saccharomyces
18	2039.5	70.2	2297	Q6BX58_DEBHA	Q6BX58 debaryomyces
19	1899.5	65.0	2273	HPAL_YEAST	Q42823 saccharomyces
20	1899.5	65.0	2273	Q42823_YEAST	Q42823 saccharomyces
21	1791	61.6	2346	Q6XDA8_HUMAN	Q6XDA8 homo sapien
22	1787	61.5	2346	Q72561_HUMAN	Q72561 homo sapien
23	1785	61.4	2345	COAL_RAT	P11497 rattus norv
24	1783	61.4	2448	Q6J1Z0_MOUSE	Q6J1Z0 mus musculus
25	1783	61.3	2345	Q5SMU9_MOUSE	Q5SMU9 mus musculus
26	1781	61.3	2346	COAL_HUMAN	Q33085 homo sapien
27	1780	61.2	2323	Q9V346_DROME	Q9V346 drosophila
28	1780	61.2	2324	COAC_CHICK	P11029 gallus gall
29	1780	61.2	2482	Q9V347_DROME	Q9V347 drosophila
30	1776	61.1	2345	Q6J1Z1_MOUSE	Q6J1Z1 mus musculus
31	1775	61.1	2346	COAL_BOVIN	Q8T563 bos taurus

32	1775	61.1	2346	1	COAL_SHEEP	Q28559 ovine aries
33	1769.5	60.9	1098	2	Q6KE89_HUMAN	Q6KE89 homo sapien
34	1769.5	60.9	2458	2	Q6KE87_HUMAN	Q6KE87 homo sapien
35	1769.5	60.9	2458	2	Q6TY48_HUMAN	Q6TY48 homo sapien
36	1767	60.8	2314	2	Q7PQ11_ANOGA	Q7PQ11 anopheles g
37	1757	60.4	1267	2	Q4SCU3_TETNG	Q4SCU3 tetradodon n
38	1716	59.0	2365	2	Q4RSU6_TETNG	Q4RSU6 tetradodon n
39	1699.5	58.5	2282	2	Q54J08_DICTDI	Q54J08 dictyosteli
40	1673.5	57.6	2456	2	Q70151_RAT	Q70151 rattus norv
41	1669.5	57.4	2456	2	COAC_HUMAN	Q00763 homo sapien
42	1604	55.2	555	1	Q6SZP8_PHYIN	Q6SZP8 phytophthor
43	1598.5	55.0	640	2	Q04849_BRANA	Q04849 brassica na
44	1598.5	55.0	1798	2	Q9FEH8_BRANA	Q9FEH8 brassica na
45	1597	54.9	2375	2	Q9FR96_ARATH	Q9FR96 arabidopsis

ALIGNMENTS

RESULT 1

Q4P514_USTMA
ID - Q4P514_USTMA PRELIMINARY; PRT; 2185 AA.

AC Q4P514;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OM04629.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelheil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Ambruster J., Bachanteang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Boukhalil M., Boukhalil B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Gierre S.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvesselis M., Karlsson E.,
RA Kells C., Kieu A., Kinser P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leiger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,
RA O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulteang Y., Topham K.,
RA Towey S., Teama T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.

RT "The genome sequence of Ustilago maydis.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACP01000168; EAK85486.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 2185 AA; 240063 MW; 8C2ECB613483DF7 CRC64;

Query Match 100.0%; Score 2907; DB 2; Length 2185;
 Best Local Similarity 100.0%; Pred. No. 2.9e-189;
 Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSKW 60
 DB 2 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSKW 61
 QY 61 AYETFGDERAIEFTVMTPELKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 120
 DB 62 AYETFGDERAIEFTVMTPELKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 121
 QY 121 GVHAWAGWGCHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
 DB 122 GVHAWAGWGCHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 181
 QY 181 PWSGTGKETMMSDQGLTVSDDDYQACIHTAEGLKAEKIGYPVMIKASGEGGKGI 240
 DB 182 PWSGTGKETMMSDQGLTVSDDDYQACIHTAEGLKAEKIGYPVMIKASGEGGKGI 241
 QY 241 RKCTNGEEFKQLYNALVGEVPGSPVFMVKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300
 DB 242 RKCTNGEEFKQLYNALVGEVPGSPVFMVKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 301
 QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPESGEFAFLELNP 360
 DB 302 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPESGEFAFLELNP 361
 QY 361 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDIRTYLGMDFRGNNEVDIDFSSPESF 420
 DB 362 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDIRTYLGMDFRGNNEVDIDFSSPESF 421
 QY 421 KTQRKPOQGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGVFSGTSGALHEYA 480
 DB 422 KTQRKPOQGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGVFSGTSGALHEYA 481
 QY 481 DSQFGHIFAYGADRSEARKQWVLSKLSIRGDFRTTVEYLKLETTAFESNKITTTGWL 540
 DB 482 DSQFGHIFAYGADRSEARKQWVLSKLSIRGDFRTTVEYLKLETTAFESNKITTTGWL 541
 QY 541 DGLIQDLRTAERPDLAV 559
 DB 542 DGLIQDLRTAERPDLAV 560

RESULT 2

Q12721 USTMA PRELIMINARY; PRT; 2185 AA.
 AC Q12721;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
 DE Acetyl CoA carboxylase (EC 6.4.1.2).
 GN Name=ACC;
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=5270;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=IMI103761;
 RC MEDLINE=96086936; PubMed=7500941; DOI=10.1007/BF00290366;
 RA Bailey A.M., Keon J.P.R., Owen J., Hargreaves J.A.;
 RT "The ACC1 gene, encoding acetyl-CoA carboxylase, is essential for

RT growth in Ustilago maydis.";
 RL Mol. Gen. Genet. 249:191-201(1995).
 DR EMBL; Z46886; CAA86983.1; -; Genomic_DNA.
 DR PIR; S60200; S60200.
 DR HSSP; Q00955; IOD4.
 DR SMR; Q12721; 11-545.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:biotin binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR011761; ATP_GRASP.
 DR InterPro; IPR011764; BC.
 DR InterPro; IPR001882; Biotin_BS.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR000022; Carboxyl_trans.
 DR InterPro; IPR011763; COA_CT_C.
 DR InterPro; IPR011762; COA_CT_N.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR005479; CPase_D2_ATP_bd.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF01039; Carboxyl_trans; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.
 DR PROSITE; PS0975; ATP_GRASP; 1.
 DR PROSITE; PS0979; BC; 1.
 DR PROSITE; PS0188; BIOTIN; UNKNOWN_1.
 DR PROSITE; PS0968; BIOTINYL_LIPOYL; 1.
 DR PROSITE; PS0989; COA_CT_CTER; 1.
 DR PROSITE; PS0980; COA_CT_NTER; 1.
 DR PROSITE; PS0866; CPASE_1; 1.
 DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
 KW Ligase.
 SQ SEQUENCE 2185 AA; 240031 MW; DCCEB709DF8EFA9 CRC64;

Query Match 99.6%; Score 2896; DB 2; Length 2185;

Best Local Similarity 99.6%; Pred. No. 1.6e-188;
 Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSKW 60
 DB 2 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAAIVKEIRSKW 61
 QY 61 AYETFGDERAIEFTVMTPELKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 120
 DB 62 AYETFGDERAIEFTVMTPELKNADYIRMDQYVEVPGGNNNNYANVDLIVDVAERA 121
 QY 121 GVHAWAGWGCHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
 DB 122 GVHAWAGWGCHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 181
 QY 181 PWSGTGKETMMSDQGLTVSDDDYQACIHTAEGLKAEKIGYPVMIKASGEGGKGI 240
 DB 182 PWSGTGKETMMSDQGLTVSDDDYQACIHTAEGLKAEKIGYPVMIKASGEGGKGI 241
 QY 241 RKCTNGEEFKQLYNALVGEVPGSPVFMVKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 300
 DB 242 RKCTNGEEFKQLYNALVGEVPGSPVFMVKLAGQARHLEVQLLADQYGNNAISIFGRDCSVQ 301
 QY 301 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPESGEFAFLELNP 360
 DB 302 RRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMWLYSPESGEFAFLELNP 361
 QY 361 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDIRTYLGMDFRGNNEVDIDFSSPESF 420
 DB 362 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDIRTYLGMDFRGNNEVDIDFSSPESF 421
 QY 421 KTQRKPOQGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGVFSGTSGALHEYA 480
 DB 422 KTQRKPOQGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGVFSGTSGALHEYA 481


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DR EMBL; AA01000031; EAL20176.1; -; Genomic_DNA.
DR SMR; Q55Q16; 24-557.
DR GO; GO:0005234; F:ATP binding; IEA.
DR GO; GO:0003374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT_N.
DR InterPro; IPR011762; COA CT_N.
DR InterPro; IPR005481; Cpsase_D2 ATP_bd.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS0975; ATP_GRASP; 1.
DR PROSITE; PS00188; Biotin; 1.
DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS0989; COA CT_CTER; 1.
DR PROSITE; PS0980; COA CT_NTER; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2237 AA; 248325 MW; A9AF395A7CA2E8E CRC64;

Query Match 78.1%; Score 2269; DB 2; Length 2237;
Best Local Similarity 77.2%; Pred. No. 1.2e-145;
Matches 429; Conservative 51; Mismatches 74; Indels 2; Gaps 1;

QY 4 DHKAVSOFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVKESIRKWAYE 63
DB 19 DHKVAQFIGNSVESAPSGRVTDFVKAHNGHTVITKVLINNGIAAIVKESIRKWAYE 78
QY 64 TFGDERAIEFTVMTATPDLKVNADYIRMAQDYVEVPGSGNNNNYANVDLVDVAERAGVH 123
DB 79 TFGSDRQIEFTVMTATPDLKVNADYIRMAQDYVEVPGSGNNNNYANVDLVDVAERAGVH 138
QY 124 AVWAGWGHAENRPLPSLAASKHKIIPGPGSAMSLGDKISSTIVAQHADVPCMPWS 183
DB 139 AVWAGWGHAENRPLPETLA--KSKIIIFGPPGSAMSLGDKISSTIVAQHAQVPCMPWS 196
QY 184 GTGKETMMSDQGLTVDVYQOACIHTAEGLKAEKIGYPMIKASGGGGKGIKRC 243
DB 197 GTGLSDITLSPQGFVTVPDKAYDDACVHSWEEGLEAEKIGFPIIMIKASGGGGKGIKRV 256
QY 244 TNGEFQKLVNAVGLVEPGSPVFMVLMAGARHLEVOLLADQYGNALISIFGRDCSVORRH 303
DB 257 EDGEKFNKSPQAVAGEVPGSPIFIMKLAGSARHLEVOLLADQYGNALISIFGRDCSVORRH 316
QY 304 QKIEEAPVTIAPEDARESMEKAARLAKLVGVYSAGTVWLVSPESGEPAFLELNPRLQ 363
DB 317 QKIEEAPVTIAPETPEEMEKAARLAKLVGVYSAGTVWLVSHSDSDSYFLELNPRLQ 376
QY 364 VEHPTEMVSGVNIIPAQLOVAMGIPLYSIRDIRTLGMPRGNEVDLDFSPSPKQTQ 423
DB 377 VEHPTEMVSGVNIIPAQLOVAMGIPLYSIRDIRTLGMPRGNEVDLDFSPSPKQTQ 436
QY 424 RKPQPGHVHVACRITAENPDTGPKPGMGALTELNFRSSTSTGWYFVSFGALHEYADSQ 483
DB 437 RKPQPGHVHVACRITAENPDTGPKPGMGALTELNFRSSTSTGWYFVSFGALHEYADSQ 496
QY 484 FGHIFAYGADRSARKOMVLSKELSTRGDFRTTVEYLIKLETDAPESNKITGWL DGL 543
DB 497 FGHIFAYGADRSARKOMVLSKELSTRGDFRTTVEYLIKLETDAPESNKITGWL DGL 556
QY 544 IQDLTAERPPADLAV 559

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DB 557 IAEGMTSERPDVAV 572
RESULT 5
O60033 EMENI
ID O60033 EMENI PRELIMINARY; PRT; 2288 AA.
AC O60033;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyl-CoA carboxylase (EC 6.4.1.2).
GN Name=acca;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A26;
RX MEDLINE=99087906; PubMed=9871120; DOI=10.1007/s002940050410;
RA Morrice J., Mackenzie D.A., Parr A.J., Archer D.B.;
RT "Isolation and characterisation of the acetyl-CoA carboxylase gene
from Aspergillus nidulans";
RL Curr. Genet. 34:379-385(1998).
DR EMBL; Y15996; CAA75926.1; -; Genomic_DNA.
DR PIR; T30568; T30568.
DR HSSP; Q00955; IOD4.
DR SNR; O60033; 21-558.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT_N.
DR InterPro; IPR011762; COA CT_N.
DR InterPro; IPR005481; Cpsase_L_N.
DR InterPro; IPR005479; Cpsase_D2 ATP_bd.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS0975; ATP_GRASP; 1.
DR PROSITE; PS0979; BC; 1.
DR PROSITE; PS00188; Biotin; 1.
DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS0989; COA CT_CTER; 1.
DR PROSITE; PS0980; COA CT_NTER; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 2288 AA; 255182 MW; 927E2518811EB1AB CRC64;

Query Match 75.3%; Score 2190; DB 2; Length 2288;
Best Local Similarity 74.8%; Pred. No. 3.1e-140;
Matches 415; Conservative 53; Mismatches 87; Indels 0; Gaps 0;

QY 5 HKAVSOFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVKESIRKWAYE 64
DB 19 HNLPSHFIGNHLDAAAPSSVKDFVANHGSHSVITSLANNNGIAAIVKESIRKWAYE 78
QY 65 FGDERAIEFTVMTATPDLKVNADYIRMAQDYVEVPGSGNNNNYANVDLVDVAERAGVHA 124
DB 79 FGNERRAIQFTVMTATPDLAANADYIRMAQDYVEVPGSGNNNNYANVELVDVAERMDVHA 138
QY 125 VWAGWGHAENRPLPSLAASKHKIIFGPPGSAMSLGDKISSTIVAQHADVPCMPWS 184

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Db 139 VWAGWGSHASENPRLESASPCKLIIFGPASAMRSLGDKISSTIVAAHQAVPCIPMSG 198
Qy 185 TGIKETMMSDQGLFTVSDVYQOACIHTABEGLEKAEKIGYVPMIKASEGGGKIRKCT 244
Db 199 TGVDEVKVDENGIVTVEEVYNGKCTFSPGEGLEKAKIGFPMIKASEGGGKIRKVE 258
Qy 245 NGEFPKQLYNAVLGVPGSPVFMKLAGOARHLEVOLLADQYGNNAISIFGRDCSVQRHQ 304
Db 259 KEEDFINLYNAANEIPSPFIMKLAGNARHLEVOLLADQYGNNISIFGRDCSVQRHQ 318
Qy 305 KIIEEAPVTIAPEDARESEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLEINPRLOV 364
Db 319 KIIEEAPVTIANPTTFQAMERAAVSLGKLVGVVSAGTVEYLYSHADDFEINPRLOV 378
Qy 365 EHPTTEMVSGVNIIPAAQLOVAMGIPLYSIRDITLYGMDPRNGNEVIDDFSSPSFKTOR 424
Db 379 EHPTTEMVTVGNLPAQLOQIANGIPLHRIIRLLYGVDPNTSAEIDDFSSPSFKTOR 438
Qy 425 KPOQGHVACRITAENPDTCFKPGMGALTEINFRSSSTWGVSFVGTSGALHEVADSOF 484
Db 439 RPQKGHTTACRITSEDPGEGFKPSGTHMELNFRSSNVWGYFVGTAGGIHFSDSOF 498
Qy 485 GHIFAYGADRSEARKQWVISKELSRGDPRTTVEYLYKLETFDAFESNKITTTGWLGLI 544
Db 499 GHIFAYGENRSASRKMVIALKELSRGDPRTTVEYLYKLETFAPFENKITTTGWLGLI 558
Qy 545 QDRLTARPPADLAV 559
Db 559 SNKLTARPPDTTIAV 573

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RESULT 6

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ID QSB004 EMENI PRELIMINARY; PRT; 2288 AA.
AC QSB004;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AN6126.2;
GN Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emericella.
OX NCBI_taxid=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fato S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jarre D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Menus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhuan P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AACD01000104; EAA58101.1; -; Genomic_DNA.

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DR SMR; QSB004; 21-558.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0009374; P:biotin binding; IEA.
DR GO; GO:0016874; P:lignase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC_1.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR011762; COA_CT_C.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; CPase_D2_ATP_bd.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS00975; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00188; BIOTIN; UNKNOWN_1.
DR PROSITE; PS00968; BIOTINYL_LIPOYL; 1.
DR PROSITE; PS00989; COA_CT_CTER; 1.
DR PROSITE; PS00980; COA_CT_NTER; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 2288 AA; 255182 MW; 927E2518811EB1AB CRC64;

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Query Match 75.3%; Score 2190; DB 2; Length 2288;
Best Local Similarity 74.8%; Pred. No. 3.1e-140;
Matches 415; Conservative 53; Mismatches 87; Indels 0; Gaps 0;
Qy 5 HKAVSQFIGNPLETAPASVADPIRQGGSHVITKVLICNNGIAAAKEIRSIKWAYET 64
Db 19 HNLPSHFIGNHLDAAAPSSVKDFVANHEGHSVITSLVLIANGIAAAKEIRSVKWAYET 78
Qy 65 FGDERAIEFTVMTATPEDLKYNADYIRNADQYVEVPGGSSNNNNYANVDLIVDVAERAGVHA 124
Db 79 FGNERAIQFTVMTATPEDLAANADYIRNADQYVEVPGGTTNNNNYANVELIVDVAERMDVHA 138
Qy 125 VWAGWGSHASENPRLESASPCKLIIFGPASAMRSLGDKISSTIVAAHQAVPCIPMSG 184
Db 139 VWAGWGSHASENPRLESASPCKLIIFGPASAMRSLGDKISSTIVAAHQAVPCIPMSG 198
Qy 185 TGIKETMMSDQGLFTVSDVYQOACIHTABEGLEKAEKIGYVPMIKASEGGGKIRKCT 244
Db 199 TGVDEVKVDENGIVTVEEVYNGKCTFSPGEGLEKAKIGFPMIKASEGGGKIRKVE 258
Qy 245 NGEFPKQLYNAVLGVPGSPVFMKLAGOARHLEVOLLADQYGNNAISIFGRDCSVQRHQ 304
Db 259 KEEDFINLYNAANEIPSPFIMKLAGNARHLEVOLLADQYGNNISIFGRDCSVQRHQ 318
Qy 305 KIIEEAPVTIAPEDARESEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLEINPRLOV 364
Db 319 KIIEEAPVTIANPTTFQAMERAAVSLGKLVGVVSAGTVEYLYSHADDFEINPRLOV 378
Qy 365 EHPTTEMVSGVNIIPAAQLOVAMGIPLYSIRDITLYGMDPRNGNEVIDDFSSPSFKTOR 424
Db 379 EHPTTEMVTVGNLPAQLOQIANGIPLHRIIRLLYGVDPNTSAEIDDFSSPSFKTOR 438
Qy 425 KPOQGHVACRITAENPDTCFKPGMGALTEINFRSSSTWGVSFVGTSGALHEVADSOF 484
Db 439 RPQKGHTTACRITSEDPGEGFKPSGTHMELNFRSSNVWGYFVGTAGGIHFSDSOF 498
Qy 485 GHIFAYGADRSEARKQWVISKELSRGDPRTTVEYLYKLETFDAFESNKITTTGWLGLI 544
Db 499 GHIFAYGENRSASRKMVIALKELSRGDPRTTVEYLYKLETFAPFENKITTTGWLGLI 558
Qy 545 QDRLTARPPADLAV 559
Db 559 SNKLTARPPDTTIAV 573

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Db 559 SNKLTARPDPTIAV 573
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Q4X1V2 ASPFU
ID Q4X1V2 ASPFU PRELIMINARY; PRT; 2292 AA.
AC Q4X1V2
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Acetyl-CoA carboxylase.
GN ORFNames=Afu2g08670;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucotales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Artzy J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feidlyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Laifon A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala J., Turner F., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000001; EAL93163.1; -; Genomic DNA.
SQ SEQUENCE 2292 AA; 254941 MW; 21624C8C5FBA7ED8 CRC64;
Query Match 75.2%; Score 2186; DB 2; Length 2292;
Best Local Similarity 74.2%; Pred No. 5, 9e-140;
Matches 412; Conservative 58; Mismatches 85; Indels 0; Gaps 0;
Qy 5 HKAVSQFTGNPLETAPASPVADPIRKGSHSVITKVLICNGIAAIVKIRKWAYET 64
Db 20 HNLPSHFTGGNHLDAAPPSSVKDFVASHEGHSVSSVLIAANGIAAIVKIRKWAYET 79
Qy 65 FGDERATEFTYMATPEDLKVADYIRMDADQVEVPGSGNNNNYANVDLIVDAERAGVHA 124
Db 80 FGNERAIOFTYMATPEDLKADYIRMDADQVEVPGSGNNNNYANVDLIVDAERAGVHA 139
Qy 125 VWAGHGHASNPRLPESLAASHKHIIIFTPPGSAMRSLGDKISSTIVAHQADVPMPWSG 184
Db 140 VWAGHGHASNPRLPESLAASHKHIIIFTPPGSAMRSLGDKISSTIVAHQAGVFCIPWSG 199
Qy 185 TGIKETWMSDGFUTVSDVVOQACIHTAEGLEKAEKIGVPMKASEGGGKIRKCT 244
Db 200 TGVDEVITIDENGIVTPDEIVKRGCTFSPERGLKKAKEIGFVPMKASEGGGKIRKVE 259
Qy 245 NGEFEKQYNALVGEVPSPPVPMKLAQAHLEVLQADQYGNALISFGDCSVORRHQ 304
Db 260 REEFISLYNAANEIPGSPFIIMKLAGNARHLEVLQADQYGNALISFGDCSVORRHQ 319
Qy 305 KIIEAPVTIAPDARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLELNPRLQV 364

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Db 320 KIIEAPVTIAPDARESMEKAAVRLAKLVGVVSAGTVEWLYSHADDFLELNPRLQV 379
Qy 365 EHPTTENVSGVNIIPAAQLQVAMGIPLYSIRDIRITLYGMDPRGNEVIDDFSSPSFKTOR 424
Db 380 EHPTTENVSGVNIIPAAQLQVAMGIPLYSIRDIRITLYGMDPRGNEVIDDFSSPSFKTOR 439
Qy 425 KPOQGHVACRITAEENPDTPGKPGMCALTTELFRSTSTWGVFSVCTSGALHEYDSOF 484
Db 440 RPOPKGHTTACRITSDPGEFGPSSGTMEHLNFRSSNWNVGFVGTAGIHSFDSOF 499
Qy 485 GHIFAYGADRSEARKOWVISKELSIKRGDPRTTVEYLKLELTDAFESNKITTWGLDGLI 544
Db 500 GHIFAYGENESASRKHMMVALKELSIKRGDPRTTVEYLKLELTDAFEDNITTWGLDGLI 559
Qy 545 QDRLTARPPADLAV 559
Db 560 SNKLTARPDPIVAV 574
RESULT 8
Q7SBL5 NEUCR
ID Q7SBL5 NEUCR PRELIMINARY; PRT; 2275 AA.
AC Q7SBL5;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU08535.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rahman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvassellis M., Mauceli E., Bielke C., Rudd S., Friehman D.,
RA Kryzofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmanli S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ABE01000166; EAA33781.1; -; Genomic DNA.
DR HSSP; P24182; 1DV1.
DR SMK; Q7SBL5; 14-558.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR011882; Biotin BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA_CT_C.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; Cpsase L N.
DR InterPro; IPR005479; Cpsase D2 ATP_bd.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.

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DR Pfam: PF01039; Carboxyl trans; 1.
DR Pfam: PF00289; CFSase_L_chain; 1.
DR Pfam: PF02786; CFSase_L_D2; 1.
DR PROSITE: PS50975; ATP_GRASP; 1.
DR PROSITE: PS50979; BC; 1.
DR PROSITE: PS00188; BIOTIN; 1.
DR PROSITE: PS50968; BIOTINYL_LIPOYL; 1.
DR PROSITE: PS50989; COA_CT_CTER; 1.
DR PROSITE: PS50980; COA_CT_CTER; 1.
DR PROSITE: PS00866; CFSASE 1; UNKNOWN 1.
DR PROSITE: PS00867; CFSASE 2; UNKNOWN 1.
DR KW Hypothetical protein.
SQ SEQUENCE 2275 AA; 254563 MW; B6A8B175C023D5BD CRC64;

Query Match 75.0%; Score 2179; DB 2; Length 2275;
Best Local Similarity 74.1%; Pred. No. 1.7e-139;
Matches 411; Conservative 57; Mismatches 87; Indels 0; Gaps 0;

Qy 5 HKAVSQFIGGNPLETAPASPVPADFTKQGGHSHVTKVLICNNGIAAIVKEIRSRKWAYET 64
Db 19 HNLAPHFIGGNPLENAPSPKVKDFVASHDGHVITVNLVIANNGIAAIVKEIRSRKWAYET 78
Qy 65 FGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHA 124
Db 79 FGDERAIEFTVMATPEDLQANADYIRMDHYYVEVPGGNNNNYANVELIVDAERMDVHA 138
Qy 125 VWAGWGHAENPRILPESLAASKHKIIFGPPGSAAMRSIGDKISSTIVAAHQADVPMPWSG 184
Db 139 VWAGWGHAENPKLPESLAASPKKIVFTGPPGSAAMRSIGDKISSTIVAAHQADVPMPWSG 198
Qy 185 TGKETWMSDGGFTVSDVVOACIHTAEGLEKAEKIGVPMKASEGGGGGKIRKCT 244
Db 199 TGVSEKVDNDNGIVTPDDVTLKGCVSQWQGLEKAREIGVPMKASEGGGGGKIRKVL 258
Qy 245 NGEBFKOLYNALVGEVPGSPVFMKLAQARHLEVQLLADQYGNIAISIFGRDCSVQRHQ 304
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Qy 305 KIIEEAPVTHAPDARESMEKAAVRLAKLVGVAGTVEWLYSPESGEFAFLELNPRLOV 364
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Qy 365 EHPTTEWMSGVNIIPAAQLQVAMGPLYISIRDIRTLGYMDPRGNEVIDFRSSPSEKFOR 424
Db 379 EHPTTEWMSGVNLPAQQLQVAMGPLYIRDIRLRLGYMDPRGNEVIDFRSSPSEKFOR 438
Qy 425 KPQPGHVYACRTAENPDTPKPGMGALTEINFRSSTSTWGYFSVGTSGALHEYADSQF 484
Db 439 RPTPKGHTTACRITSEDPGEGFKPSNGVLHDLNFRSSNVNMGVFSVGSAGGIHSPDSQF 498
Qy 485 GHIFAYGADRSEARKQWVSKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSI 544
Db 499 GHIFAYGENAARSKRMVVALKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSI 558
Qy 545 QDRLTAEPRPADLAV 559
Db 559 SKLTAERPDPIAV 573

RESULT 9
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AC Q51YC2;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORNames=MG07613.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]

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NUCLEOTIDE SEQUENCE.

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RP STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RA Bayul T., Blitshetyn B., Bloom T., Blye J., Boguelavskiy L.,
RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gierke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hgopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyselis M., Karlsson E.,
RA Kells C., Kleu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McGhee T., Meldrim J., Menes L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Menga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settupalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talama J., Tchuanga P.,
RA Tenzing P., Tefaye S., Theodore J., Thoultsang Y., Topham K.,
RA Tovey S., Teamlu T., Tsomo N., Vallée D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01000922; EAA53336.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 2344 AA; 262098 MW; E2FE164E451733D6 CRC64;

Query Match 74.4%; Score 2163; DB 2; Length 2344;
Best Local Similarity 73.5%; Pred. No. 2.3e-138;
Matches 408; Conservative 59; Mismatches 88; Indels 0; Gaps 0;

Qy 5 HKAVSQFIGGNPLETAPASPVPADFTKQGGHSHVTKVLICNNGIAAIVKEIRSRKWAYET 64
Db 38 HKIADHFIGGNPLENAPSPKVKSWAHDGHTVITVNLVIANNGIAAIVKEIRSRKWAYET 97
Qy 65 FGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHA 124
Db 98 FGDERAIEFTVMATPEDLQANADYIRMDHYYVEVPGGNNNNYANVELIVDAERMDVHA 157
Qy 125 VWAGWGHAENPRILPESLAASKHKIIFGPPGSAAMRSIGDKISSTIVAAHQADVPMPWSG 184

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Db 158 VWAGWGHASNPPLPESLAAPKIIIFIGPPGSAMRSLGDKISSTIVQAHAQVPCIPWSG 217
 Qy 185 TGIKETWMSDQGFITVSDVYQACIHTABEGLEKABKIGYPVMIKASEGGGKIRKCT 244
 Db 218 TGVDVAQIDKKGIVTVDDTYAKGCVTSWEGLEKARQIGFPVMIKASEGGGKIRKAV 277
 Qy 245 NGEFFKOLYNVAVLGEVPGSPVFMKLAGOARHLEVOALLDOYGNNAISIFGRDCSVORRHQ 304
 Db 278 SEEGFELYKAAASEIPGSPFIMKLAGNARHLEVOALLDOYGNNAISIFGRDCSVORRHQ 337
 Qy 305 KIIEEAPVTIAPEDARESMKAAVRLAKLVYVSAGTVEWLYSPESGEFAFLEINPRLQV 364
 Db 338 KIIEEAPVTIAPEDARESMKAAVRLAKLVYVSAGTVEWLYSHADDDKFFLEINPRLQV 397
 Qy 365 EHPTTEWMSGVNIPAAQLQVAMGIPLYSIIRDTLYGMDPRGNEVIDDFSSPESFQTR 424
 Db 398 EHPTTEWMSGVNIPAAQLQVAMGIPLYSIIRDTLYGMDPRGNEVIDDFSSPESFQTR 457
 Qy 425 KPOQGHVACRITAEENPDGTGFKPGMGALTENFRSSTWGYFSVGTSGALHEYADSO 484
 Db 458 RPSKGLHTACRITSEDPGEGFKPSNGVMHLEINFRSSNVWGYFSVGTSGALHEYADSO 517
 Qy 485 GHIPAYGADRSEARKQWISLKELSIIRGDFRTTVEYLIKLETFDAFESNKITTTGWLGLI 544
 Db 518 GHIPAYGENRSASRKNVIALKELSIIRGDFRTTVEYLIKLETFDAFESNKITTTGWLGLI 577
 Qy 545 QDRLTARPPADLAV 559
 Db 578 SKCLTARPPDKMLAV 592

RESULT 10

Q41878 GIBZE PRELIMINARY; PRT; 2271 AA.
 ID Q41878 GIBZE PRELIMINARY; PRT; 2271 AA.
 AC Q41878;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG06580.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Menues L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.
 DR EMBL; AACM01000259; EAA78365.1; -, Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 2271 AA; EC40D82850B76583 CRC64;
 Query Match 73.9%; Score 2148; DB 2; Length 2271;
 Best Local Similarity 72.4%; Pred. No. 2.3e-137;
 Matches 403; Conservative 64; Mismatches 90; Indels 0; Gaps 0;
 Qy 3 PDHVASQFIGNPLETAPSPADPIRQGGHSHVITKVLICNNGIAAAYKEIRSIKRWAY 62
 Db 18 PYFNIAIDHEFIGNRLNAPSGVKDFVQNDGHTVITNVLNANGIAAAYKEIRSVKRWAY 77
 Qy 63 ETPGDERAETPTMATPEDLKUNADYIRNADQYVEVPGSSNNNNYANVDLIIVDAVRAGV 122
 Db 78 ETPGDERAETPTMATPEDLOANAEYIRNADHYVEVPGTNNHNYANVELIIVDAERMNV 137
 Qy 123 HAVWAGWGHASNPPLPESLAAPKIIIFIGPPGSAMRSLGDKISSTIVQAHAQVPCIPW 182
 Db 138 HAVWAGWGHASNPPLPESLAAPKIIIFIGPPGSAMRSLGDKISSTIVQAHAQVPCIPW 197
 Qy 183 SGTGKETWMSDQGFITVSDVYQACIHTABEGLEKABKIGYPVMIKASEGGGKIRK 242
 Db 198 SGTGVDQVAVDDKIGIVTVADDIYAQCVTSWEGLEKAKEIGFPVMIKASEGGGKIRK 257
 Qy 243 CTNGEPEFKOLYNVAVLGEVPGSPVFMKLAGOARHLEVOALLDOYGNNAISIFGRDCSVOR 302
 Db 258 ATEEGFEALYKAAASEIPGSPFIMKLAGNARHLEVOALLDOYGNNAISIFGRDCSVOR 317
 Qy 303 HOKIIEEAPVTIAPEDARESMKAAVRLAKLVYVSAGTVEWLYSPESGEFAFLEINPRL 362
 Db 318 HOKIIEEAPVTIAPEDARESMKAAVRLAKLVYVSAGTVEWLYSHADDDKFFLEINPRL 377
 Qy 363 QVEHPTEWMSGVNIPAAQLQVAMGIPLYSIIRDTLYGMDPRGNEVIDDFSSPESFXT 422
 Db 378 QVEHPTEWMSGVNIPAAQLQVAMGIPLYSIIRDTLYGMDPRGNEVIDDFSSPESFXT 437
 Qy 423 QRPQPOGHVACRITAEENPDGTGFKPGMGALTENFRSSTWGYFSVGTSGALHEYADS 482
 Db 438 QRPQPOGHVACRITAEENPDGTGFKPGMGALTENFRSSTWGYFSVGTSGALHEYADS 497
 Qy 483 QFCHIPAYGADRSEARKQWISLKELSIIRGDFRTTVEYLIKLETFDAFESNKITTTGWL 542
 Db 498 QFCHIPAYGENRSASRKNVIALKELSIIRGDFRTTVEYLIKLETFDAFESNKITTTGWL 557
 Qy 543 LIQDRLTARPPADLAV 559
 Db 558 LISKRLTARPPDKMLAV 574

RESULT 11

Q6CL34 KULULA PRELIMINARY; PRT; 2231 AA.
 ID Q6CL34 KULULA PRELIMINARY; PRT; 2231 AA.
 AC Q6CL34;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|Q00955|Saccharomyces cerevisiae YNR016c ACC1 acetyl-CoA
 DE carboxylase.
 GN OrderedLocusNames=KLLA0F06072g;
 OS Kluyveromyces lactis (Yeast);
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,


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DR PROSITE; PS50989; COA_CT_CTER; 1.
DR PROSITE; PS50980; COA_CT_CTER; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 2233 AA; 250049 MW; 8B381EA1F3C99FC3 CRC64;

Query Match          71.9%; Score 2090.5; DB 2; Length 2233;
Best Local Similarity 70.7%; Pred. No. 1.9e-133;
Matches 391; Conservative 73; Mismatches 86; Indels 3; Gaps 2;

QY 9 SQFIGGNPLETAPASPVADPFIRKOGSHSVITKVLICNNGIAAIVKAEIRSKWAEYFQDE 68
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 30 SHFVGLTVKVEDSPLEKFEVKAHGHHVIVSKVLIAANGIAAIVKAEIRSKWAEYFQDE 89
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 69 RAIEFTVMATPEDLVNADYIRMDQVVEVPGSGNNNNYANVDLIVDAERAGVHAWAG 128
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 90 KIVQFVAMATPEDLEANAAYIRMDQVVEVPGGTNNNNYANVDLIVDAERADVDWAG 149
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 129 WGHASENPRLPESLAASKHIIIFGPGSGMRSGLGDKISSTIVAQAHDVPCMPWSGTGK 188
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 150 WGHASENPRLPEKLARKSKRILFTGPPGNMRSGLGDKISSTIVAQAHAQVPCIPWSGTGV- 208
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 189 ETWMSDQ--GFLTVDSDVQOACHTAEGLKAEKIGYPMVMIKASGGGKGIRKCTNG 246
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 209 DTVIDKNGLVSDDDIYQKCCSPEDGLEKAKIGFPMVMIKASGGGKGIRQVIRE 268
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 247 EEFKQLYNAVILGVEPGSFVFMKLAGQARHLEVLQALLADQYGNATISIFGRDCSVQRHQKI 306
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 269 EDFNLVHQAAEIPGSPFIMKLAKGRHLEVLQALLADQYGNATISIFGRDCSVQRHQKI 328
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 307 IEAPVTIAPEDARESEKAARLAKLVGVTSAGTVLEWLYSPESGEPFLELPRLOVEH 366
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 329 IEAPVTIAPETFGMEKAARLVKLVGVTSAGTVLEWLYSHDDNKFYFLELPRLOVEH 388
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 367 PTTEMVSGVNIIPAQLQVAMGIPLYSDIRTLVGMDPGRNEVIDPDPSPSPFKTORKP 426
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 389 PTTEMVGVNLPAQLQVAMGIPWHRISDIRIFGLNPRSSSEIDFEKSEDSLKTORQP 448
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 427 QPQGVHVACITAEINPDTPKPGMGALTELNFRSSSTWGYVSGTSGALHEYADSQFGH 486
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 449 IPKGHCTACRITSEDPNDGPKPSGGTLNELNFRSSNVWGYVSGNGGIIHSFSDSQFGH 508
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 487 IPAYGADRSEARQWYLSIKELSTRGDFRTVEYLKILKLEDAFESKNITTHGLDGLIQD 546
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 509 IFAFGENRQSRKHMVVALKELSTRGDFRTVEYLKILKLEDAFESKNITTHGLDGLIST 568
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 547 RLTAERPPADLAV 559
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 569 KMTAKRPDPLAV 581
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
COAC_SCHPO STANDARD; PRT: 2280 AA.
AC P78820; Q09447; Q09576; Q09616; Q09667;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Acetyl-CoA:carboxylase (EC 6.4.1.2) (ACC) (Cell untimely torn protein
DE 6) [includes: Biotin carboxylase (EC 6.3.4.14)].
GN Name:cut6; ORFName:SPAC56E4.04c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=972 / HM123;
RA Saito A., Kazuta Y., Toh H., Kondo H., Tanabe T.;
RT "Biotin-dependent enzymes in Schizosaccharomyces pombe: cloning and
RT nucleotide sequences of acetyl-CoA carboxylase and pyruvate

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carboxylase.";
Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Williams R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellag T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
RA James K.D., Jones I., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moutie S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
RA Hillbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
[3]
RP NUCLEOTIDE SEQUENCE OF 14-161; 636-871; 998-1098 AND 1380-1547.
RX MEDLINE=96354912; PubMed=8769419; DOI=10.1083/jcb.134.4.949;
RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
RA Hirata A., Yanagida M.;
RT "Aberrant mitosis in fission yeast mutants defective in fatty acid
RT synthetase and acetyl CoA carboxylase.";
RL J. Cell Biol. 134:949-961 (1996).
CC -!- FUNCTION: This protein carries three functions: biotin carboxyl
CC carrier protein, biotin carboxylase, and carboxyltransferase.
CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate
CC + malonyl-CoA.
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
CC -!- COFACTOR: Biotin.
CC -!- ENZYME REGULATION: By phosphorylation (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
CC step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Contains 1 ATP-grasp domain.
CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.
CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.
CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D78169; BAAL1238.1; -; Genomic DNA.
CC EMBL; Z99261; CAB16395.1; -; Genomic DNA.
CC EMBL; D83413; BAAL1914.1; -; Genomic DNA.
CC EMBL; D83414; BAAL1915.1; -; Genomic DNA.
CC EMBL; D83416; BAAL1917.1; -; Genomic DNA.
CC EMBL; D83415; BAAL1916.1; -; Genomic DNA.
CC FIR; T38906; T38906.
CC HSSP; Q00955; IOD4.
CC GeneDB Spombe; SPAC56E4.04c; -.
CC GO; GO:000920; P:cell separation during cytokinesis; IMP.
CC GO; GO:0007059; P:chromosome segregation; IMP.

```



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DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR011761; ATP_GRASP.
DR InterPro: IPR011764; BC.
DR InterPro: IPR001882; Biotin BS.
DR InterPro: IPR005482; Biotin carb C.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000022; Carboxyl_trans.
DR InterPro: IPR011763; COA CT_C.
DR InterPro: IPR011762; COA CT_N.
DR InterPro: IPR005481; CPase D2 ATP_bd.
DR InterPro: IPR005479; CPase L_N.
DR Pfam: PF02785; Biotin carb C; 1.
DR Pfam: PF00364; Biotin_lipoyl; 1.
DR Pfam: PF01039; Carboxyl_trans; 1.
DR Pfam: PF00289; CPase L_chain; 1.
DR Pfam: PF02786; CPase L_D2; 1.
DR PROSITE: PS0979; BC; 1.
DR PROSITE: PS0975; ATP_GRASP; 1.
DR PROSITE: PS00188; BIOTIN; UNKNOWN 1.
DR PROSITE: PS0968; BIOTINYL_LIPOYL; 1.
DR PROSITE: PS0989; COA CT_NTER; 1.
DR PROSITE: PS0980; COA CT_CTER; 1.
DR PROSITE: PS0866; CPASE_1; UNKNOWN 1.
DR PROSITE: PS0867; CPASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 2266 AA; 251115 MW; 8581AF5F9374E4A CRC64;

Query Match 71.7%; Score 2084; DB 2; Length 2266;
Best Local Similarity 71.2%; Pred. No. 5.4e-133;
Matches 399; Conservative 63; Mismatches 96; Indels 2; Gaps 2;

QY 2 PPHKAV-SQIFGNPLETAPASVADPIRKGHSHVITKVLICNNGIAAIVKESIRKWK 60
DB 30 PNIHKLASHFFGLNSVHTAKPSKVEFVASHGHTVINKVLIANNGIAAIVKESIRKWK 89
QY 61 AYETFGDERALEFTVMTAPEDLKVNADYIRMDQYVEVPGSGNNNNYANDVLVDVAERA 120
DB 90 AYETFGDERAISFTVMTAPEDLANADYIRMDQYVEVPGSGNNNNYANDVLVDVAERF 149
QY 121 GVHVAWAGWGHASNPRLPSLAASHKHIIFFIGPPGSAESLGDKISSTIVAQHADVPCM 180
DB 150 GVDVAWAGWGHASNPRLPSLAASPRKIVFIGPPGSAESLGDKISSTIVAQHAKVPCI 209
QY 181 PWSGTGKETNM-SDQGLTVSDDDVYQOACIHTAEGLKAEKIGYVPMIKASEGGGKG 239
DB 210 PWSGTGVDEVVVDKSTNLVSSEVYTKGTTGPKQGLERAKQIGPPVMIKASEGGGKG 269
QY 240 IRKCTNGEEFKOLYNVLGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSV 299
DB 270 IRKVEREEDPEAAHQVEGIPSPFIMQLAGNARHLEVQLLADQYGNALISIFGRDCSV 329
QY 300 QRHQKILIEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTVSEWLYSPESGEFAFLELN 359
DB 330 QRHQKILIEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTVSEWLYSHEDDKFYFLELN 389
QY 360 PRLOVEHPTTMTSGVNVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSPES 419
DB 390 PRLOVEHPTTMTSGVNVNIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSPES 449
QY 420 FKTORKPOGHVAVACHITAEINPDTPGKPGMGALTELFNFRSSSTWGYFSVGTSGALHEY 479
DB 450 DKTORREVPVPGHTTACRITSEDPEGEKPGSGTGMHLEFNFRSSSNVMGVYFVGNGQGHISF 509
QY 480 ADSOFGHIFAYGADRSARKOMVLSIKELSGIRGDFRTTVEYLKLELTDAPFNKLTGW 539
DB 510 SDQFGHIFAFGENRSARKOMVLSIKELSGIRGDFRTTVEYLKLELTDAPFNKLTGW 569
QY 540 LDGLIQRLTAERPPADLAV 559
DB 570 LDELISNKLTAERPPDSFLAV 589
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RESULT 15
Q7SEK8 ASHGO
ID Q7SEK8 ASHGO PRELIMINARY; PRT; 2231 AA.
AC Q7SEK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AAR071WP.
GN Name=AAR071W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
DR EMBL: AE016814; AAS50436.1; -: Genomic_DNA.
DR SHR: Q7SEK8; 16-566, 1480-2216.
DR AGD; AAR071W; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0009374; F:biotin binding; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR011761; ATP_GRASP.
DR InterPro: IPR011764; BC.
DR InterPro: IPR001882; Biotin BS.
DR InterPro: IPR005482; Biotin carb C.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000022; Carboxyl_trans.
DR InterPro: IPR011763; COA CT_C.
DR InterPro: IPR011762; COA CT_N.
DR InterPro: IPR005479; CPase D2 ATP_bd.
DR Pfam: PF02785; Biotin carb C; 1.
DR Pfam: PF00364; Biotin_lipoyl; 1.
DR Pfam: PF01039; Carboxyl_trans; 1.
DR Pfam: PF00289; CPase L_chain; 1.
DR Pfam: PF02786; CPase L_D2; 1.
DR PROSITE: PS0979; BC; 1.
DR PROSITE: PS0975; ATP_GRASP; 1.
DR PROSITE: PS00188; BIOTIN; 1.
DR PROSITE: PS0968; BIOTINYL_LIPOYL; 1.
DR PROSITE: PS0989; COA CT_CTER; 1.
DR PROSITE: PS0980; COA CT_NTER; 1.
DR PROSITE: PS0866; CPASE_1; UNKNOWN 1.
DR PROSITE: PS0867; CPASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 2231 AA; 249717 MW; 5024EA7C7873B842 CRC64;

Query Match 71.2%; Score 2069.5; DB 2; Length 2231;
Best Local Similarity 70.4%; Pred. No. 5.2e-132;
Matches 387; Conservative 71; Mismatches 91; Indels 1; Gaps 1;

QY 11 FIGGNPLETAPASVADPIRKGHSHVITKVLICNNGIAAIVKESIRKWAYETFGDERA 70
DB 32 FIGLNTVEQAEASPLRDYVRLHGHTVITSKILLIANNGIAAIVKESIRKWAYETFGDGKV 91
QY 71 IEFTVMTAPEDLKVNADYIRMDQYVEVPGSGNNNNYANDVLVDVAERAGVHVAWAGW 130
DB 92 VQFVMTAPEDLEANTEYIRMDQYVEVPGSGNNNNYANDVLVDVAERADVDVAWAGW 151
QY 131 HASENPRLPSLAASHKHIIFFIGPPGSAESLGDKISSTIVAQHADVPCMPWSGTGKET 190
DB 152 HASENPRLPSLAASHKHIIFFIGPPGSAESLGDKISSTIVAQHAKVPCIPWSGTGVDQV 211
QY 191 MMSDQ-GFLTVDSDVYQOACIHTAEGLKAEKIGYVPMIKASEGGGKGIRKCTNGEFP 249
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Db 212 EIDPHTKLVSADIIYQKCCCLSPEDGLNKAQKIGFFVWVKAASGGGKGIRKVVREDF 271
Qy 250 KQLNVLGEVPGSPVFMKLAGQARHLEVLQADQYNAISIFGRDCSVORRHQKIIIE 309
Db 272 ISLYQQAANEIPGSPIFITMKLAGARHLEVLQADQYTNISLFGDCSVORRHQKIIIE 331
Qy 310 APVTIAPEDARESMEKAARLAKLVGVYSAGTVEWLYSPESGEFAFLELNPRLQVEHPT 369
Db 332 APVTIAPEDTTPAEMERAAVRIGKLVGVYSAGTVEYLYSHEEDKPYFLELNPRLQVEHPT 391
Qy 370 EMVSGVNIAPQAQLOVAMGIPLYSIRDITLYGMPDPRGNEVIDDFPSGESPKTKQPOQ 429
Db 392 EMVTGVNLPAQAQLOIANGIPLHRIRDLFLGLDPHTATEIDFESSADALQTORRPIPK 451
Qy 430 GHVVACRITARNPDTGPKPGMGALTELNFRSTSTWGYFVSGTSGALHEYADSQGHIFA 489
Db 452 CHCTACRITSDPNEGKPGSGSLHFNFRSSNVWGYFVSGNGGIHSFSDSQGHIFA 511
Qy 490 YGADRSARKOMVLSKELSRGDFRTTVEYLKILETDAFESKNITTGWLGLDGLIQRILT 549
Db 512 FGENRQSRKHVMVVALKELSRGDFRTTVEYLKILETDEPDNTITTGWLDDLISQKIS 571
Qy 550 AERPPADLAV 559
Db 572 AEKDPDLAV 581

RESULT 16
Q5AAM4 CANAL
ID Q5AAM4 CANAL PRELIMINARY; PRT; 2271 AA.
AC Q5AAM4
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein ACC1.
GN Name=ACC1; ORFNames=CaO19.7466;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federpiet N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AAC001000039; EAK99708.1; -; Genomic_DNA.
DR SRR; Q5AAM4; 60-606.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; F:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; AC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl_trans.
DR InterPro; IPR011763; COA_CT_N.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; CPease_L_N.

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DR InterPro; IPR005479; CPease_D2_ATP_bd.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl_trans; 1.
DR Pfam; PF00289; CPease_L_chain; 1.
DR Pfam; PF02786; CPease_L_D2; 1.
DR PROSITE; PS00975; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00188; BIOTIN; UNKNOWN_1.
DR PROSITE; PS00968; BIOTINYL_LIPOYL; 1.
DR PROSITE; PS00989; COA_CT_CTER; 1.
DR PROSITE; PS00980; COA_CT_NTER; 1.
DR PROSITE; PS00866; CPease_1; 1.
DR PROSITE; PS00867; CPease_2; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2271 AA; 253422 MW; D57D403C36D7A290 CRC64;

Query Match 70.9%; Score 2061.5; DB 2; Length 2271;
Best Local Similarity 70.7%; Pred. No. 1.9e-131;
Matches 390; Conservative 63; Mismatches 98; Indels 1; Gaps 1;

Qy 9 SQFIGGNPLETAPASPVADPIRKQGHGSHVITKVLICNNGIAAIVEKIRSKWAYETFGDE 68
Db 70 SHEFGNGLNABSPSKVRDFVRAHQGHTVTSKLIANNGLIAAIVEKIRSKWAYETFGDE 129
Qy 69 RAIEFTVMATPEDLKVNADYIRNADQYVEVPGSSNNNNYANVDLIYDVAERAGVHAYWAG 128
Db 130 KAIQFTVMATPEDLEANAERYNADQFIEVPGGTNNNNYANVDLIYVEIAESTNAHAYWAG 189
Qy 129 WGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGK 188
Db 190 WGHASENPLPEKLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQAHAQVFCIPWSGTGVD 249
Qy 189 ETWMSDQ-GFLTVDVDDVYQOACHTAPEGLEKAEKIGYPVMIKASGGGKGIRKCTNGE 247
Db 250 EVKIDPQTNLVSADDIYAKGCTSPEDGLEKAKIGFPMIKASGGGKGIRKVDDEK 309
Qy 248 EFQQLNVLGEVPGSPVFMKLAGQARHLEVLQADQYNAISIFGRDCSVORRHQKII 307
Db 310 NFITLYNQAAANEIPGSPIFITMKLAGARHLEVLQADQYTNISLFGDCSVORRHQKII 369
Qy 308 EAPVTIAPEDARESMEKAARLAKLVGVYSAGTVEWLYSPESGEFAFLELNPRLQVEHP 367
Db 370 EAPVTIARKETHEMENAAVRIGKLVGVYSAGTVEYLYSHEEDKPYFLELNPRLQVEHP 429
Qy 368 TTEMVSGVNIAPQAQLOVAMGIPLYSIRDITLYGMPDPRGNEVIDDFPSGESPKTKQKP 427
Db 430 TTEMVTVGNLPAQAQLOIANGIPMHRIRDLITLYGADPHTTTDIDFEFKSETSLVSQRPT 489
Qy 428 PQGHVACRITARNPDTGPKPGMGALTELNFRSTSTWGYFVSGTSGALHEYADSQGH 487
Db 490 PKGCHTACRITSDPNEGKPGSGSLHFNFRSSNVWGYFVSGNGGIHSFSDSQGH 549
Qy 488 FAYGADRSARKOMVLSKELSRGDFRTTVEYLKILETDAFESKNITTGWLGLDGLIQR 547
Db 550 FAFGENRQSRKHVMVVALKELSRGDFRTTVEYLKILETDEPDNTITTGWLDELITKK 609
Qy 548 LTAERPPADLAV 559
Db 610 LTAERPPDPIVAV 621

RESULT 17
COAC YEAST
ID COAC YEAST STANDARD; PRT; 2233 AA.
AC Q00955;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin
DE carboxylase (EC 6.3.4.14)].
GN Name=FA33; Synonyms=ACC1; OrderedLocusNames=YNR016C; ORFNames=N3175;
OS Saccharomyces cerevisiae (Baker's yeast).

```

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCB1_TaxID=4932;
 RN (1)
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 2015-2022.
 RP MEDLINE=92262474; PubMed=1350093;
 RA Al-Feel W., Chirala S.S., Wakil S.J.;
 RT "Cloning of the yeast *PAS3* gene and primary structure of yeast acetyl-
 RT CoA carboxylase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4534-4538 (1992).
 RN (2)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP MEDLINE=97313269; PubMed=9169873;
 RA Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,
 RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
 RA Beinhauer J.D., Boskovic J., Butirago M.J., Bussereau F., Coster F.,
 RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,
 RA Daignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
 RA Fritz C., Gallard C., Garcia-Cantalejo J.M., Glandsdorff N.,
 RA Goffeau A., Gueidener U., Herbert C.J., Heumann K., Heusdens-Neitzel D.,
 RA Halbert H., Hinni K., Iragui Housaini I., Jacquet M., Jimenez A.,
 RA Joniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
 RA Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,
 RA Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,
 RA Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,
 RA Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,
 RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
 RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhaesselt P.,
 RA Vierendeels F., Viessers S., Voet M., Volckaert G., Wach A.,
 RA Wambutt R., Wedler H., Zollner A., Hani J.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIV
 RT and its evolutionary implications.";
 RL Nature 387:93-98 (1997).
 RN (3)
 RP PHOSPHORYLATION SITE SRR-1157.
 RP MEDLINE=21864552; PubMed=11875433; DOI=10.1038/nbt0302-301;
 RA Picarro S.B., McClelland M.L., Stukenberg P.T., Burke D.J., Ross M.M.,
 RA Shabanowitz J., Hunt D.F., White F.W.;
 RT "Phosphoproteome analysis by mass spectrometry and its application to
 RT *Saccharomyces cerevisiae*.";
 RL Nat. Biotechnol. 20:301-305 (2002).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1429-2233 IN COMPLEX WITH
 RP COA, MUTAGENESIS OF LEU-1705; ARG-1731; TRP-1738 AND ARG-1954, AND
 RP HOMODIMERIZATION.
 RP PubMed=12663926; DOI=10.1126/science.1081366;
 RA Zhang H., Yang Z., Shen Y., Tong L.;
 RT "Crystal structure of the carboxyltransferase domain of acetyl-
 RT coenzyme A carboxylase.";
 RL Science 299:2064-2067 (2003).
 CC -1- FUNCTION: This protein carries three functions: biotin carboxyl
 CC carrier protein, biotin carboxylase, and carboxyltransferase.
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 CC + malonyl-CoA.
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -1- COFACTOR: Biotin.
 CC -1- ENZYME REGULATION: By phosphorylation.
 CC -1- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
 CC step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Contains 1 ATP-grasp domain.
 CC -1- SIMILARITY: Contains 1 biotin carboxylation domain.
 CC -1- SIMILARITY: Contains 1 biotinyl-binding domain.
 CC -1- SIMILARITY: Contains 1 carboxyltransferase domain.
 CC -1- SIMILARITY: Contains 1 carboxyltransferase domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC ENBL; M92156; AAA20073.1; -; Unassigned DNA.
 DR ENBL; Z71631; CAA96294.1; -; Genomic DNA.
 DR PIR; S63347; S63347.
 DR PDB; 1OD2; X-ray; A/B=1429-2233.
 DR PDB; 1OD4; X-ray; A/B/C=1429-2233.
 DR PDB; 1U9R; X-ray; A/B=1482-2218.
 DR PDB; 1UYS; X-ray; A/B/C=1482-2218.
 DR PDB; 1UYT; X-ray; A/B=.
 DR PDB; 1UYV; X-ray; A/B=.
 DR PDB; 1W2X; X-ray; A/B/C=1476-2233.
 DR PDB; 1W93; X-ray; A=14-566.
 DR PDB; 1W96; X-ray; A/B/C=13-566.
 DR SMR; Q00955; 14-566.
 DR InterAct; Q00955; -.
 DR GeneOnline; 143361; -.
 DR Ensembl; YNR016C; *Saccharomyces cerevisiae*.
 DR SGD; S00005299; ACC1.
 DR GO; GO:0005789; Cytoplasmic reticulum membrane; IDA.
 DR GO; GO:0005739; Cytoplasmic reticulum membrane; IDA.
 DR GO; GO:0003989; Fatty acid biosynthesis; IMP.
 DR GO; GO:0004075; Fatty acid biosynthesis; IMP.
 DR GO; GO:0006998; P-nuclear membrane organization and biogenesis; TAS.
 DR GO; GO:0006506; P-protein-nucleus import; IMP.
 DR InterPro; IPR011761; ATP GRASP.
 DR InterPro; IPR011761; BC.
 DR InterPro; IPR001882; Biotin BS.
 DR InterPro; IPR005482; Biotin carb C.
 DR InterPro; IPR000089; Biotin lipoyl.
 DR InterPro; IPR000022; Carboxyl trans.
 DR InterPro; IPR011763; COA CT C.
 DR InterPro; IPR011762; COA CT N.
 DR InterPro; IPR005481; CPase L N.
 DR InterPro; IPR005479; CPase D2 ATP bd.
 DR Pfam; PF02785; Biotin carb C; 1.
 DR Pfam; PF00364; Biotin lipoyl; 1.
 DR Pfam; PF01039; Carboxyl trans; 1.
 DR Pfam; PF00289; CPase L chain; 1.
 DR Pfam; PF02786; CPase L D2; 1.
 DR PROSITE; PS00975; ATP GRASP; 1.
 DR PROSITE; PS00979; BC; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00968; BIOTINYL LIPOYL; 1.
 DR PROSITE; PS00989; COA CT CTER; 1.
 DR PROSITE; PS00980; COA CT NTER; 1.
 DR PROSITE; PS00866; CPASE 1; 1.
 DR PROSITE; PS00867; CPASE 2; 1.
 DR 3D-structure; ATP-binding; Biotin; Complete proteome;
 KW Direct protein sequencing; Fatty acid biosynthesis; Ligase;
 KW Lipid synthesis; Multifunctional enzyme; Nucleotide-binding;
 KW Phosphorylation.
 FT DOMAIN 58 567 Biotin carboxylation.
 FT DOMAIN 216 408 ATP-grasp.
 FT DOMAIN 701 767 Biotinyl/lipoyl.
 FT DOMAIN 1603 2101 Carboxyltransferase.
 FT NP_BIND 236 261 ATP (By similarity).
 FT ACT_SITE 383 383 By similarity.
 FT BINDING 735 735 Biotin (covalent) (By similarity).
 FT BINDING 1731 1731 Coenzyme A.
 FT BINDING 2034 2034 Coenzyme A.
 FT BINDING 2036 2036 Coenzyme A.
 FT MOD_RES 1157 1157 Phosphoserine.
 FT MUTAGEN 1705 1705 L->I: Raises Km for malonyl-CoA by a factor of 20.
 FT MUTAGEN 1731 1731 R->S: Raises Km for malonyl-CoA by a factor of 15.
 FT MUTAGEN 1738 1738 Y->F: No effect.
 FT MUTAGEN 1954 1954 R->S: Raises Km for malonyl-CoA by a factor of 70.
 FT MUTAGEN 1994 1994 E->Q: Lowers activity 10-fold.
 FT CONFLICT 1523 1523 W -> G (in Ref. 1).
 FT CONFLICT 1755 1755 I -> IYRCL (in Ref. 1).
 FT CONFLICT 1761 1766 AINQML -> ESTNA (in Ref. 1).

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SQ SEQUENCE 2233 AA; 250353 MW; 0A335AARD9B1F8308 CRC64;
Query Match 70.9%; Score 2060; DB 1; Length 2233;
Best Local Similarity 69.1%; Pred. No. 2.3e-131;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

QY 3 PDHKAVSQFIGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKWAY 62
DB 29 PGH-----FIGLTVKLEESPLRDFVXSHGHGHTVISKILIANNGIAAVKEIRSIRKWAY 83

QY 63 ETFGDERAIEFTVMATPEDLKVNADYIRMAQYVEVPGGSSNNNNYANVDLIVDAERAGV 122
DB 84 ETFGDRTVQVAMATPEDLEANAIEYIRMAQYIEVPGGTNNNNYANVDLIVDAERADV 143

QY 123 HAVWAGHASENPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAOHADVPCMPW 182
DB 144 DAVWAGHASENPLLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAOHADVPCMPW 203

QY 183 SGTGIGKETSMDQ--GFLTVSDVDVYQACIHTAEGLKAEKIGYPMWIKASEGGGGKI 240
DB 204 SGTGV-DTVHVDKTLVSDVDVYQACIHTAEGLKAEKIGYPMWIKASEGGGGKI 262

QY 241 RKCTNGEEFKOLYNALVEVPGSPVFMVKLAGQARHLEVQLLADQYGNASIFGRDCSVQ 300
DB 263 ROVEREDFIYALHQANEIPGSPFIMVKLAGRARHLEVQLLADQYGNASIFGRDCSVQ 322

QY 301 RRHOKIIEAPVTIAPEDARESMEKAARVLAKLVGYVSAGTVEMLYSPESGEFAFLNLP 360
DB 323 RRHOKIIEAPVTIAPEDARESMEKAARVLAKLVGYVSAGTVEMLYSHDDGKFYFLNLP 382

QY 361 RLQVEHPTTEMVSGVNPAPQALQVAMGIPLYSIDITLYGMDPRGNEVIDDFESSPEF 420
DB 383 RLQVEHPTTEMVSGVNPAPQALQVAMGIPLYSIDITLYGMDPRGNEVIDDFESSPEF 442

QY 421 KTORKPOQHGVVACRITAEINPDTGPKPGMGALTELFNFRSSTSTWGVSVGTSGALHEYA 480
DB 443 KQRRPPIPKGCHTACRITSEDPNDGPKPGSGTLHFNFRSSNVGVSVGTSGALHEYA 502

QY 481 DSQFGHIPAYGADSEARSKQWISLKSIRSGDRFTTVEYLKLETTAFESNKITITGWL 540
DB 503 DSQFGHIPAYGADSEARSKQWISLKSIRSGDRFTTVEYLKLETTAFESNKITITGWL 562

QY 541 DGLIQDRLTAERPPADLAV 559
DB 563 DDLITHKQWTAEXPDPTLAV 581

RESULT 18
Q6BX58 DEBHA
ID Q6BX58 DEBHA PRELIMINARY; PRT; 2297 AA.
AC Q6BX58;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to CA5816|CaAC1 Candida albicans CaAC1 acetyl-coenzyme-A
DE carboxylase.
GN OrderedLocNames=DEHA0B05632g;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1].
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

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RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382134; CAG85206.1; -; Genomic_DNA.
DR SWR; Q6BX58; 79-628; 1547-2257.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; F:metabolism; IEA.
DR InterPro; IPR011761; ATP_GASP.
DR InterPro; IPR011764; BC_.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT C.
DR InterPro; IPR011762; COA CT N.
DR InterPro; IPR005481; CPase L N.
DR InterPro; IPR005479; CPase D2 ATP bd.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; CPase L chain; 1.
DR Pfam; PF02786; CPase L D2; 1.
DR PROSITE; PS00975; ATP_GASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS00989; COA CT NTER; 1.
DR PROSITE; PS00980; COA CT NTER; 1.
DR PROSITE; PS00866; CPASE_1; UNKNOWN 1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN 1.
KW Complete proteome.
SQ SEQUENCE 2297 AA; 257947 MW; 0E766966B5C4CB33 CRC64;

Query Match 70.2%; Score 2039.5; DB 2; Length 2297;
Best Local Similarity 69.4%; Pred. No. 6.1e-130;
Matches 385; Conservative 72; Mismatches 97; Indels 1; Gaps 1;

QY 6 KAVSQFIGNPLETAPASPVADFIKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET 65
DB 89 KLADHEFKGLNSADNAEPKVTDFVRSHEGHTVLSRVLIANNGLAIAVKEIRSVKWAYET 148

QY 66 GDERAIEFTVMATPEDLKVNADYIRMAQYVEVPGGSSNNNNYANVDLIVDAERAGVAV 125
DB 149 GDERAIEFTVMATPEDLEANAIEYIRMAQYIEVPGGTNNNNYANVDLIVDAERTNVDAV 208

QY 126 WAGWGHASENPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAOHADVPCMPHSGT 185
DB 209 WAGWGHASENPLLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAOHADVPCIPMSGT 268

QY 186 GIKETWMSDQ--GFLTVSDVDVYQACIHTAEGLKAEKIGYPMWIKASEGGGGKIRKCT 244
DB 269 GYREVKIDETNLVSDVAVYAKGCTSPEDGLVKAKEIGFPWIKASEGGGGKIRKVD 328

QY 245 NGEFKQLYNALVEVPGSPVFMVKLAGQARHLEVQLLADQYGNASIFGRDCSVQRHQ 304
DB 329 NEKDFIALYKQASNEIPGSPFIMVKLAGDARHLEVQLLADQYGNASIFGRDCSVQRHQ 388

QY 305 KIIIEAPVTIAPEDARESMEKAARVLAKLVGYVSAGTVEMLYSPESGEFAFLNPRLOV 364
DB 389 KIIIEAPVTIAPEDARESMEKAARVLAKLVGYVSAGTVEMLYSHSBDKPYFLNPRLOV 448

QY 365 EHPPTWMSGVNIPAAQLQVAMGIPLYSIDITLYGMDPRGNEVIDDFESSPEFQTOR 424
DB 449 EHPPTWMSGVNIPAAQLQVAMGIPLYSIDITLYGMDPRGNEVIDDFESSPEFQTOR 508

QY 425 KPQPGHVVACRITAEINPDTGPKPGMGALTELFNFRSSTSTWGVSVGTSGALHEYADSQF 484

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Db 509 RVPKGGHTTACITSEDEGEGFKPGGSLHFNFRSSNVMGYFVGNGQSSIHFSQSOF 568
Qy 485 GHIFAYGADRSEARKOWISLKELSGIRGDFRTTVYLYKLLETFDAFESNKITTWGLDGLI 544
Db 569 GHIFAFGENSRASRKHVVALKELSGIRGDFRTTVYLYKLLETFDPDNTITTWGLDELI 628
Qy 545 QDRLTAERPPADLAV 559
Db 629 SKKLTSERPDHIVAV 643

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RESULT 19

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HFAL YEAST
ID HFAL1 YEAST STANDARD; PRT; 2273 AA.
AC P32874;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE HFAL protein.
GN Name=HFAL; OrderedLocusNames=YMR207C; ORFNames=YMR261.01C, YMR325.08C;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_taxid=4932;
RN (1)
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor K., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lyne G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII."
RL Nature 387:90-93 (1997).
RN (2)
NUCLEOTIDE SEQUENCE OF 125-949.
RX MEDLINE=94146412; PubMed=7906156;
RA Kearsey S.E.;
RT "Identification of a Saccharomyces cerevisiae gene closely related to
RT FAS3 (acetyl-CoA carboxylase).";
RL DNA Seq. 4:69-70 (1993).
CC -!- COFACTOR: Biotin (By similarity).
CC -!- SIMILARITY: Contains 1 ATP-grasp domain.
CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.
CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.
CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.
CC -!- CAUTION: The reading frame from which this protein is translated
CC has no Met initiation codon near to the 5' end. It does not seem to
CC be a pseudogene. There are no apparent frameshifts.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z49809; CA889922.1; -; Genomic DNA.
CC EMBL; Z48755; CA88647.1; -; Genomic DNA.
CC EMBL; Z22558; CA80280.1; -; Genomic DNA.
CC PIR; S55089; S55089.
CC HSSP; Q00955; 10D4.
CC SMR; P32874; 90-634.
CC GenOnline; 142882; -.
CC SGB; S000004820; HFAL.
CC GO; GO:0005739; Mitochondrion; IDA.
CC GO; GO:0003989; Fatty acid biosynthesis; IGI.
CC GO; GO:0006633; Fatty acid biosynthesis; IGI.
CC InterPro; IPR011761; ATP_GRASP.
CC InterPro; IPR011764; BC.
CC InterPro; IPR001882; Biotin_BS.

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DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA_CT_C.
DR InterPro; IPR011762; COA_CT_N.
DR InterPro; IPR005481; Cpsase_L_N.
DR InterPro; IPR005479; Cpsase_D2_ATP_bd.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS00975; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00968; BIOTINYL_LIPOYL; 1.
DR PROSITE; PS00989; COA_CT_CTER; 1.
DR PROSITE; PS00980; COA_CT_NTER; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW ATP-binding; Biotin; Complete proteome; Ligase; Nucleotide-binding.
FT DOMAIN 134 635
FT DOMAIN 292 484
FT DOMAIN 770 836
FT DOMAIN 1648 2147
FT NP_BIND 332 337
FT ACT_SITE 459 459
FT BINDING 804 804
FT CONFLICT 661 661
SQ SEQUENCE 2273 AA; 259163 MW; 08727A301549DA92 CRC64;
Query Match 65.0%; Score 1889.5; DB 1; Length 2273;
Best Local Similarity 64.3%; Pred. No. 1.1e-119;
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps 4;
Qy 2 PPDHKAVSQFICGNPLETASPVPADPIKQGGHSHVTKVLICNNGTAAYKEIERSIKWA 61
Db 105 PP-----QFGLNTVESAQFSILRDFVLRGGHTVISKILIANNGIAAVKEMRSIRKA 158
Qy 62 YETFGDERALEFTVMTATPEDLVKNADYIRIMADQVEVPGGNNNNYANVDLIVDAERAG 121
Db 159 YETFNDEKILQFVVMATPDDLHANSEYIRIMADQVQVPGGTNNNNYANIDLILDAEQTD 218
Qy 122 VHAWAGWGHASNPRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAHQADVPOMP 181
Db 219 VDAVWAGWGHASNPCLPELLASSQRKILFIPGPPGRMRSLGDKISSTIVAAQSAKIPICP 278
Qy 182 WSGTGIKETWMSDQ--GFLTVDVDDVYQACIHTAEGLKAEKIGYPMVMIKASGGGGKG 239
Db 279 WSGSHI--DTTHIDNKNFVSPDDVYVYRGCCSPEDALEKAKLIGFPMVMIKASGGGGKG 337
Qy 240 IRKCTNGEEFKQLYNAVLGVPVGVPMKLAGQARHLEVQLLADQYGNATISIFGRDCSV 299
Db 338 IRRVDNEDDIFALYRQAVNETPGSPFMVVKVTDARHLEVQLLADQYGNATITLFGDCSI 397
Qy 300 QRRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVYAGTVEMLYSPSGEGFAFELN 359
Db 398 QRRHQKIIIEAPVTITKPTETFORMERAAIRLGLVGVYAGTVBYLYSPKDDKVFYFLELN 457
Qy 360 PRLOVEHPTTEMVSGVNIIPAAQLQVANGIPLYSTRDITLYGMDPRGNEVIDDFSSPES 419
Db 458 PRLQVEHPTTEMISGVNLPATQLQIANGIPMHMISDKILYGLDPTQTSYID----- 509
Qy 420 FKTORKPOQGHVHVACRITAEENPDTPGKPGMGALTTELNFRSSTSTWGYFVSGTSGALHEY 479
Db 510 FKILKRPSPKCHCISCRITSEDNNEGKPKSTGKIHELNFSSSNVWGYFVSGNGAIHSF 569
Qy 480 ADSQFGHIFAYGADRSEARKOWISLKELSGIRGDFRTTVYLYKLLETFDAFESNKITTW 539
Db 570 SDSQFGHIFAYGADRQDAKQNMVVALKELSGIRGDFRTTVYLYKLLETFDAFESNISTGW 629
Qy 540 LDGLIQDRLTAE 551

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Db 630 LDDLLKLNSSD 641
RESULT 20
O42823 YEAST PRELIMINARY; PRT; 2273 AA.
AC O42823;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyl-coenzyme A carboxylase (Fragment).
GN Name=ALC;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SPI;
RA Saito A., Kazuta Y., Kondo H., Tanabe T.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78465; BA24410.1; -; Genomic_DNA.
DR HSSP; Q00955; 10D4.
DR SMR; O42823; 90-634.
DR Ensembl; YMR207C; Saccharomyces cerevisiae.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPRO11761; ATP_GRASP.
DR InterPro; IPRO11764; BC.
DR InterPro; IPRO01982; Biotin BS.
DR InterPro; IPRO05482; Biotin_carb C.
DR InterPro; IPRO00089; Biotin_lipoyl.
DR InterPro; IPRO00022; Carboxyl trans.
DR InterPro; IPRO11763; COA CT C.
DR InterPro; IPRO11762; COA CT N.
DR InterPro; IPRO05481; Cpsase L N.
DR InterPro; IPRO05479; Cbp_synch_L_D2.
DR Pfam; PF02785; Biotin_carb C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; Cpsase L chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS0975; ATP_GRASP; 1.
DR PROSITE; PS0979; BC; 1.
DR PROSITE; PS0188; Biotin; 1.
DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS0989; COA CT CTER; 1.
DR PROSITE; PS0980; COA CT NTER; 1.
DR PROSITE; PS0866; Cpsase_1; UNKNOWN_1.
DR PROSITE; PS0867; Cpsase_2; UNKNOWN_1.
KW Biotin.
FT NON TER
SQ SEQUENCE 2273 AA; 259162 MW; BF6C01982FCB5DEF CRC64;

Query Match 65.0%; Score 1889.5; DB 2; Length 2273;
Best Local Similarity 64.3%; Pred. No. 1.le-119;
Matches 355; Conservative 86; Mismatches 94; Indels 17; Gaps 4;

QY 2 PPDKAVSOFIIGGNPLETAPASPVADPIRKOGHSHVTKVLICNGIAAVKEIRSIKWA 61
Db 105 PP-----QFGLNVTSAQPSILRDFVDRGGHTVSKILIANNGIAAVKEIRSIKWA 159
QY 62 YETFGDERAIEFTVMATPEDELKVADYIRMAQVVEPVGSGNNNNYANVDLIVDAERAG 121
Db 159 YETFENDEKILQFVMAFPDHLHANSEYIRMAQVQVPGTNNNNYANIDLILDVAEQTD 218
QY 122 VHAWAGWGHASENPRIPESLAASKHILFIPTGPGSARSLGDKISSTIVAQAHDVPCMP 181
Db 219 VDVAWAGWGHASENPFCLPELLASSQKILFIPTGPGRAMRSLGDKISSTIVAQAQAKIFCIP 278
QY 182 WSGTGIKETWMSDQ--GFLTIVSDVYQQAICHTAEGLKAEKGIYPWMIKASGGGGKG 239

Db 279 WSGSHI-DTIIHNKTNFVSPDDVYVRGCCSSPEDALEKAKLIGFPPMIKASGGGGKG 337
QY 240 IRKCTNGEEFKQLYNVLGEVPGSPFVFMKLAGARHLEVLQADQYGNALISIFGRDCSV 299
Db 338 IRRVDNEDDFALYRQAVNETPGSPFMVFMKVVTDAHLEVLQADQYGTNTITLFGDCSI 397
QY 300 QRRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWEVLYSPESGEFAFLN 359
Db 398 QRRHQKIIIEAPVTITKPTFORMERAAIRLGLVGVYSAGTVBYLYSPKDDKFFYLEIN 457
QY 360 PRLOVEHPTTEMVSGVNIIPAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFESSPE 419
Db 458 PRLOVEHPTTEMISGVNLPATQLQIAMGIPMHMISDKLYGLDPTGTSYID----- 509
QY 420 FKORKEPQOGHVVACRITAEINPDTGPKPGMGALTEINFRSSTSTWGYFSVGTSGALHEY 479
Db 510 FKNLKRPSKGCISCRTSDEDPNEGKFPSTGKIHELNFSSSNVWGYFSVGNNGAIHSP 569
QY 480 ADSQFGHIFAYGADRSEARKOMVLSKELSIKELSIKELSIKELSIKELSIKELSIKELSI 539
Db 570 SDSQFGHIFAVGNDRQDAKQNMVLAKDFSIKELSIKELSIKELSIKELSIKELSIKELSI 629
QY 540 LDGLIQDLRTAE 551
Db 630 LDDLLKLNSSD 641

RESULT 21
O6XDA8 HUMAN
ID O6XDA8 HUMAN PRELIMINARY; PRT; 2346 AA.
AC O6XDA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Acetyl-CoA carboxylase alpha.
GN Name=ACACA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Snitnikova O.M., Ginolhac S.M., Magnard C., Leone M., Anczukow O.,
RA Moreau K., Thompson D., Coutanson C., Bonadona V., Lasset C.,
RA Goldgar D.E., Joulin V., Dalla Venezia N., Lenoir G.M.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY237919; AAF69841.1; -; mRNA.
DR Ensembl; ENSG00000132142; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPRO11761; ATP_GRASP.
DR InterPro; IPRO11764; BC.
DR InterPro; IPRO01982; Biotin BS.
DR InterPro; IPRO05482; Biotin_carb C.
DR InterPro; IPRO00089; Biotin_lipoyl.
DR InterPro; IPRO00022; Carboxyl trans.
DR InterPro; IPRO11763; COA CT C.
DR InterPro; IPRO11762; COA CT N.
DR InterPro; IPRO05481; Cpsase L N.
DR InterPro; IPRO05479; Cpsase_D2 ATP_bd.
DR Pfam; PF02785; Biotin_carb C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.
DR Pfam; PF02786; Cpsase_L_D2; 1.
DR PROSITE; PS0975; ATP_GRASP; 1.
DR PROSITE; PS0979; BC; 1.
DR PROSITE; PS0188; BIOTIN; 1.
DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.

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DR PROSITE; PS50989; COA_CT_CTER; 1.
 DR PROSITE; PS50980; COA_CT_NTER; 1.
 DR PROSITE; PS00866; CPASE 1; 1.
 DR PROSITE; PS00867; CPASE 2; UNKNOWN 1.
 SQ SEQUENCE 2346 AA; 265554 MW; F1FOA518F8824FFC CRC64;

Query Match 61.6%; Score 1791; DB 2; Length 2346;
 Best Local Similarity 63.8%; Pred. No. 6e-113; Indels 14; Gaps 5;
 Matches 345; Conservative 79; Mismatches 103;

QY 22 ASPVADFIKQGGHSVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 81
 DB 103 ASP-AEFVTRFGNGKVIKVLIANNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 161

QY 82 LKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVAVWAGHGHASENPRLPES 141
 DB 162 LKANAEYIKMAHYVVPVPGGPNNNYANVELLDIAKIPVQAVWAGHGHASENPKLP 221

QY 142 LAASKHKIIFIPGSGAMRSIGDKISSTIVAQHADVPKMPWGTGKETMMSD---QGFL 198
 DB 222 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSLRVDMQENDFSKRIL 279

QY 199 TVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258
 DB 280 NVPQELYEKGVKVDVDDGLQAAEEVGPVMIKASEGGGKGIRKVNADDPNLPFRQVQA 339

QY 259 EVPGPSVFMKLAGARHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPVTIAPED 318
 DB 340 EVPGPSPIFVMLAKQSRHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPATIATPA 399

QY 319 ARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFALELNPRLQVEHPTTEMVSGVNP 498
 DB 512 SENDEGFKPSSGTQVELNFRSNKNVWGYFSVAAAGGLHEFADSFQGHCFSGNGENREAI 571

QY 499 KQWISLKELSIKRGDFTTVEYLKLETDAPESNKITGWDGLIQDLRTAERPADLA 558
 DB 572 SNMVALKELSIKRGDFTTVEYLKLETDAPESNKITGWDGLIQDLRTAERPADLM 631

QY 559 V 559
 DB 632 V 632

RESULT 22

Q7Z561 HUMAN
 ID Q7Z561 HUMAN PRELIMINARY; PRT; 2346 AA.
 AC Q7Z561
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Acetyl-CoA carboxylase 1.
 GN Name=ACCL1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Adipocyte;
 RX MEDLINE=22709197; PubMed=12810950; DOI=10.1073/pnas.1332670100;
 RA Mao J., Chirala S.S., Wakil S.J.;
 RT "Human acetyl-CoA carboxylase 1 gene: presence of three promoters and
 RT heterogeneity at the 5'-untranslated mRNA region."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7515-7520(2003).

DR EMBL; AY315627; AAP94122.1; -; mRNA.
 DR HSSP; F24182; IDV1.
 DR Ensembl; ENSG00000132142; Homo sapiens.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:biotin binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR011761; ATP_GRASP.
 DR InterPro; IPR011764; BC.
 DR InterPro; IPR001882; Biotin_BS.
 DR InterPro; IPR005482; Biotin carb C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR000022; Carboxyl trans.
 DR InterPro; IPR011763; COA_CT_C.
 DR InterPro; IPR011762; COA_CT_N.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR005479; CPase_D2_ATP_bd.
 DR Pfam; PF02785; Biotin carb C; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF01039; Carboxyl trans; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.
 DR PROSITE; PS50975; ATP_GRASP; 1.
 DR PROSITE; PS50979; BC; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS50968; BIOTINYL_LIPOYL; 1.
 DR PROSITE; PS50989; COA_CT_CTER; 1.
 DR PROSITE; PS50980; COA_CT_NTER; 1.
 DR PROSITE; PS00866; CPASE_1; 1.
 DR PROSITE; PS00867; CPASE_2; UNKNOWN 1.
 SQ SEQUENCE 2346 AA; 265615 MW; AC156BCBD15F77AB CRC64;

Query Match 61.5%; Score 1787; DB 2; Length 2346;
 Best Local Similarity 63.6%; Pred. No. 1.1e-112;
 Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

QY 22 ASPVADFIKQGGHSVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 81
 DB 103 ASP-AEFVTRFGNGKVIKVLIANNGIAAIVKESIRKWAYETFGDERAIEFTVMATPED 161

QY 82 LKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVAVWAGHGHASENPRLPES 141
 DB 162 LKANAEYIKMAHYVVPVPGGPNNNYANVELLDIAKIPVQAVWAGHGHASENPKLP 221

QY 142 LAASKHKIIFIPGSGAMRSIGDKISSTIVAQHADVPKMPWGTGKETMMSD---QGFL 198
 DB 222 LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSLRVDMQENDFSKRIL 279

QY 199 TVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNALVG 258
 DB 280 NVPQELYEKGVKVDVDDGLQAAEEVGPVMIKASEGGGKGIRKVNADDPNLPFRQVQA 339

QY 259 EVPGPSVFMKLAGARHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPVTIAPED 318
 DB 340 EVPGPSPIFVMLAKQSRHLEVQLLADQYGNALISIFGRDCSVORRHQKIEEAPATIATPA 399

QY 319 ARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFALELNPRLQVEHPTTEMVSGVNP 378
 DB 400 VFEHEQCAVRLAKLVGVVSAGTVEYLIS-QDGSFYFLELNPRLQVEHPTTEMVADVNP 458

QY 379 AAQQLQVAMGIPLYSIRDIRTLTGMDPRNGNEVIDFDFSSPESFKTKQKPOQHVVACRIT 438
 DB 459 AAQQLQVAMGIPLYRIKDIRMVGSPWGDSPIDFDSA-----HVPKPRGHVIAARIT 511

QY 439 AENPDGFKPGMGALTELNFRSSTTWGYSFVGTSGALHEYADSFQGHIFAYGADRSEAR 498
 DB 512 SENDEGFKPSSGTQVELNFRSNKNVWGYFSVAAAGGLHEFADSFQGHCFSGNGENREAI 571

QY 499 KQWISLKELSIKRGDFTTVEYLKLETDAPESNKITGWDGLIQDLRTAERPADLA 558
 DB 572 SNMVALKELSIKRGDFTTVEYLKLETDAPESNKITGWDGLIQDLRTAERPADLM 631

QY 559 V 559
 DB 632 V 632

Db 632 V 632

RESULT 23

COAL RAT STANDARD; PRT; 2345 AA.

AC P11497; P97902;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)]

GN Name=Acaca; Synonyms=Acac;

OS Rattus norvegicus (Rat)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Muridae; Rattus.

OX NCBI_TaxID=10116;

[1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RP MEDLINE=89320328; PubMed=2901088;

RA Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M.A., Kim K.-H.;

RT "Structure of the coding sequence and primary amino acid sequence of acetyl-coenzyme A carboxylase.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:5784-5788 (1988).

[2]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RP MEDLINE=89264558; PubMed=2566999;

RA Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.;

RT "Structural features of the acetyl-CoA carboxylase gene: mechanisms for the generation of mRNAs with 5' end heterogeneity.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046 (1989).

[3]

RP NUCLEOTIDE SEQUENCE OF 1-33.

RP MEDLINE=89214151; PubMed=2565337;

RA Lopez-Casillas F., Kim K.-H.;

RT "Heterogeneity at the 5' end of rat acetyl-coenzyme A carboxylase mRNA. Lipogenic conditions enhance synthesis of a unique mRNA in liver.";

RL J. Biol. Chem. 264:7176-7184 (1989).

[4]

RP NUCLEOTIDE SEQUENCE OF 1167-1200 (ISOFORMS 1 AND 2), AND PHOSPHORYLATION SITE SR-1200.

RP MEDLINE=90337981; PubMed=1974251;

RA Kong I.-S., Lopez-Casillas F., Kim K.-H.;

RT "Acetyl-CoA carboxylase mRNA species with or without inhibitory coding sequence for Ser-1200 phosphorylation.";

RL J. Biol. Chem. 265:13695-13701 (1990).

[5]

RP BIOTIN-BINDING SITE.

RP MEDLINE=89289706; PubMed=2567668;

RA Bai D.-H., Moon T.-W., Lopez-Casillas F., Andrews P.C., Kim K.-H.;

RT "Analysis of the biotin-binding site on acetyl-CoA carboxylase from rat.";

RL Eur. J. Biochem. 182:239-245 (1989).

[6]

RP PROTEIN SEQUENCE OF 76-85 AND 1198-1201, AND PHOSPHORYLATION.

RP MEDLINE=88296498; PubMed=2900138;

RA Munday M.R., Campbell D.G., Carling D., Hardie D.G.;

RT "Identification by amino acid sequencing of three major regulatory phosphorylation sites on rat acetyl-CoA carboxylase.";

RL Eur. J. Biochem. 175:331-338 (1988).

[7]

RP PARTIAL PROTEIN SEQUENCE, AND MASS SPECTROMETRY.

RP STRAIN=Mistar; TISSUE=Liver;

RP MEDLINE=94237850; PubMed=7910165;

RA Wenz R., Hess D., Bebersold R., Brownsey R.W.;

RT "Unique structural features and differential phosphorylation of the 280-kDa component (isozyme) of rat liver acetyl-CoA carboxylase.";

RL J. Biol. Chem. 269:14438-14445 (1994).

CC -I- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and carboxyltransferase.

CC -I- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.

CC -I- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -I- COPACTOR: Biotin.

CC -I- ENZYME REGULATION: By phosphorylation.

CC -I- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting) step.

CC -I- SUBCELLULAR LOCATION: Cytoplasmic.

CC -I- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Names=1;

CC IsoId=P11497-1; Sequence=Displayed;

CC Names=2;

CC IsoId=P11497-2; Sequence=VSP_011753;

CC -I- PTM: The N-terminus is blocked.

CC -I- SIMILARITY: Contains 1 ATP-grasp domain.

CC -I- SIMILARITY: Contains 1 biotin carboxylation domain.

CC -I- SIMILARITY: Contains 1 biotinyl-binding domain.

CC -I- SIMILARITY: Contains 1 carboxyltransferase domain.

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CC -----

CC EMBL; J03808; AAA40653.1; -; mRNA.

CC EMBL; M28731; AAA40652.1; -; Genomic DNA.

CC EMBL; M26195; AAA40654.1; -; mRNA.

CC EMBL; M26196; AAA40655.1; -; mRNA.

CC EMBL; M26197; AAA40656.1; -; mRNA.

CC EMBL; M55315; -; NOT_ANNOTATED_CDS; mRNA.

CC PIR; A35378; A35578.

CC HSP; Q00955; I0D4.

CC Ensembl; ENSRNOG0000034013; Rattus norvegicus.

CC RGD; 621248; Acac.

CC InterPro; IPR011761; ATP_GRASP.

CC InterPro; IPR011764; BC.

CC InterPro; IPR001882; Biotin_BS.

CC InterPro; IPR005482; Biotin_carb_C.

CC InterPro; IPR000089; Biotin_lipoyl.

CC InterPro; IPR000022; Carboxyl_trans.

CC InterPro; IPR011763; COA_CT_C.

CC InterPro; IPR011762; COA_CT_N.

CC InterPro; IPR005481; CPase_I_N.

CC InterPro; IPR005479; CPase_D2_ATP_bd.

CC Pfam; PF02785; Biotin_carb_C; 1.

CC Pfam; PF00364; Biotin_lipoyl; 1.

CC Pfam; PF01039; Carboxyl_trans; 1.

CC Pfam; PF00289; CPase_L_chain; 1.

CC Pfam; PF02786; CPase_L_D2; 1.

CC PROSITE; PS00975; ATP_GRASP; 1.

CC PROSITE; PS00979; BC; 1.

CC PROSITE; PS00188; BIOTIN; 1.

CC PROSITE; PS00968; BIOTINYL_LIPOYL; 1.

CC PROSITE; PS00989; COA_CT_CTER; 1.

CC PROSITE; PS00980; COA_CT_NTER; 1.

CC PROSITE; PS00866; CPASE_1; 1.

CC PROSITE; PS00867; CPASE_2; 1.

CC Alternative splicing; ATP-binding; Biotin; Direct protein sequencing;

CC Fatty acid biosynthesis; Ligase; Lipid synthesis;

CC Multifunctional enzyme; Nucleotide-binding; Phosphorylation.

CC DOMAIN 116 617 Biotin carboxylation.

CC DOMAIN 274 465 ATP-grasp.

CC DOMAIN 751 817 Biotinyl/lipoyl.

CC DOMAIN 1697 2193 Carboxyltransferase.

CC NP_BIND 314 319 ATP (Potential).

CC ACT_SITE 440 440 By similarity.

CC BINDING 785 785 Biotin (covalent).

FT BINDING 1822 1822 Coenzyme A (By similarity).
FT BINDING 2126 2126 Coenzyme A (By similarity).
FT BINDING 2128 2128 Coenzyme A (By similarity).
FT MOD_RES 77 77 Phosphoserine.
FT MOD_RES 79 79 Phosphoserine.
FT MOD_RES 1200 1200 Phosphoserine.
FT VARSPIC 1189 1196 Missing (in isoform 2).
FT SEQUENCE 2345 AA, 265194 MW, 7895CF9ADEIE8771 CRC64;
Query Match 61.4%; Score 1785; DB 1; Length 2345;
Best Local Similarity 63.6%; Pred. No. 1.5e-112;
Matches 344; Conservative 80; Mismatches 103; Indels 14; Gaps 5;
QY 22 ASPVADPIKQGHSHVITKVLICNNGIAAVKIRKWAYETFGDERAIEFTVMATPED 81
DB 102 ASP-AEFVTRFGNGKVIKVLINNGIAAVKIRKWAYETFGDERAIEFTVMATPED 160
QY 82 LKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGWGHASENPRLPES 141
DB 161 LKANAEYIKWADHYVPPGGANNNTANVELLIDIAKRIIPVQAVWAGWGHASENPRLPES 220
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAHADVPCMPWSTGTGKETMMSD---QGFL 198
DB 221 LL--KNGIAFMGPPSQAMWALGDKIASIVAGTAGITPLPWSGSLRVDMQENDFSKRIL 278
QY 199 TVSDDDVYQQAACHTAEGLKAEKIGYPVMIKASGGGGKIRKCTNGEEFKOLYNVILG 258
DB 279 NVPOQLYKGYKVDVDDGLKAAEEVGPVMIKASGGGGKIRKVNADDFNLPFQVQA 338
QY 259 EYVPGSPVFMKLAGQARHLEVLQADQYGNALSIKGRDCSVORRHOKIIEEAPVTIAPED 318
DB 339 EYVPGSPVFMKLAGQARHLEVLQADQYGNALSIKGRDCSVORRHOKIIEEAPVTIAPED 398
QY 319 ARSEMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLEINPRLQVEHPTTEMVSGVNI 378
DB 399 VFEHMEQCAVLAKWGVYVSAGTVEWLYS-QDGSFYFLEINPRLQVEHPTTEMVSGVNI 457
QY 379 AAQLQVAMGIPLYSIRDIRTYLGMGRNEVIDFDPSSESPKTKQKPOQGHVACRIT 438
DB 458 AAQLQVAMGIPLYSIRDIRTYLGMGRNEVIDFDPSSESPKTKQKPOQGHVACRIT 510
QY 439 AENPDGFGKPGCALTEINFRSTSTWGYFSVGTSGALHEYADSPGHIFAYGADRSEAR 498
DB 511 SENPDGFGKPGCALTEINFRSTSTWGYFSVGTSGALHEYADSPGHIFAYGADRSEAR 570
QY 499 KQWVLSKELSIKRGDPRFTTVEYLKLETDAPESNKITTCGLDGLIQDLRTAERPPADIA 558
DB 571 SNMVALKELSIKRGDPRFTTVEYLKLETDAPESNKITTCGLDGLIQDLRTAERPPADIA 630
QY 559 V 559
DB 631 V 631

RESULT 24

Q6JIZO MOUSE PRELIMINARY; PRT; 2448 AA.
AC Q6JIZO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Acetyl-CoA carboxylase 2.
GN Name=Acacb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Mao J., Wakil S.J.;

RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451394; AAS13686.1; -; mRNA. complex; IEA.
DR GO; GO:0009343; C:biotin carboxylase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR005482; Biotin carb. C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT C.
DR InterPro; IPR011762; COA CT N.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; Cmp synth_L_D2.
DR InterPro; IPR002114; HPr Serp_S.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS0975; ATP GRASP; 1.
DR PROSITE; PS0979; BC; 1.
DR PROSITE; PS0968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS0989; COA CT CTER; 1.
DR PROSITE; PS0980; COA CT NTER; 1.
DR PROSITE; PS0866; CPASE 1; UNKNOWN 1.
DR PROSITE; PS0867; CPASE 2; UNKNOWN 1.
DR PROSITE; PS0589; PTS HPR SER; UNKNOWN 1.
SQ SEQUENCE 2448 AA, 275666 MW, 0B8649F5D2CF1C8A CRC64;

Query Match 61.4%; Score 1783.5; DB 2; Length 2448;

Best Local Similarity 63.8%; Pred. No. 2.1e-112;

Matches 346; Conservative 73; Mismatches 108; Indels 15; Gaps 7;

QY 22 ASPVADPIKQGHSHVITKVLICNNGIAAVKIRKWAYETFGDERAIEFTVMATPED 81
DB 235 ASP-AEFVTRFGNGKVIKVLINNGIAAVKIRKWAYETFGDERAIEFTVMATPED 293
QY 82 LKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGWGHASENPRLPES 141
DB 294 LKANAEYIKWADHYVPPGGANNNTANVELLIDIAKRIIPVQAVWAGWGHASENPRLPES 353
QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAHADVPCMPWSTGTGKETMMSD---QG-F 197
DB 354 LC--KHEIAFLGPPSEAMWALGDKIASIVAGTAGITPLPWSGSLRVDMQENDFSKRIL 411
QY 198 LTVSDDDVYQQAACHTAEGLKAEKIGYPVMIKASGGGGKIRKCTNGEEFKOLYNVIL 257
DB 412 ISVPEDVYEQGVKVDVDEGLQAAEKIGYPVMIKASGGGGKIRKCTNGEEFKOLYNVIL 471
QY 258 GEVPGSPVFMKLAGQARHLEVLQADQYGNALSIKGRDCSVORRHOKIIEEAPVTIAPED 317
DB 472 SEIPGSPVFMKLAGQARHLEVLQADQYGNALSIKGRDCSVORRHOKIIEEAPVTIAPED 531
QY 318 DARSEMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLEINPRLQVEHPTTEMVSGVNI 377
DB 532 AVSEFMEQCAVLAKWGVYVSAGTVEWLYS-RDGSFHFLEINPRLQVEHPTTEMVSGVNI 590
QY 378 AAQLQVAMGIPLYSIRDIRTYLGMGRNEVIDFDPSSESPKTKQKPOQGHVACRIT 437
DB 591 AAQLQVAMGIPLYSIRDIRTYLGMGRNEVIDFDPSSESPKTKQKPOQGHVACRIT 643
QY 438 TAENPDGFGKPGCALTEINFRSTSTWGYFSVGTSGALHEYADSPGHIFAYGADRSEAR 497
DB 644 TSENPDGFGKPGCALTEINFRSTSTWGYFSVGTSGALHEYADSPGHIFAYGADRSEAR 703
QY 498 KQWVLSKELSIKRGDPRFTTVEYLKLETDAPESNKITTCGLDGLIQDLRTAERPPADIA 557
DB 704 ISNMVALKELSIKRGDPRFTTVEYLKLETDAPESNKITTCGLDGLIQDLRTAERPPADIA 763
QY 558 AV 559

Db 558 ELSIRGDFRTTVEYLITLLETRNFRFLDNSIDTAWLDALIAERVQSEKPDILLGV 610

RESULT 28

COAC_CHICK STANDARD; PRT; 2324 AA.

AC P11029;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin carboxylase (EC 6.3.4.14)].

GN Name=ACAC;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

RN [1]_TaxID=9031;

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=88139305; PubMed=2893793;

RA Takai T., Yokoyama C., Wada K., Tanabe T.;

RT "Primary structure of chicken liver acetyl-CoA carboxylase deduced from cDNA sequence."

RL J. Biol. Chem. 263:2651-2657(1988).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 493-820.

RC TISSUE=Liver;

RX MEDLINE=87106011; PubMed=2879745; DOI=10.1016/0014-5793(87)81564-8;

RA Takai T., Wada K., Tanabe T.;

RT "Primary structure of the biotin-binding site of chicken liver acetyl-CoA carboxylase."

RL FEBS Lett. 212:98-102(1987).

CC -!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and carboxyltransferase.

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate + malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- COPACTOR: Biotin.

CC -!- ENZYME REGULATION: By phosphorylation.

CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting) step.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Contains 1 ATP-grasp domain.

CC -!- SIMILARITY: Contains 1 biotin carboxylation domain.

CC -!- SIMILARITY: Contains 1 biotinyl-binding domain.

CC -!- SIMILARITY: Contains 1 carboxyltransferase domain.

CC -----

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CC -----

DR EMBL; J03541; AAA48701.1; -; mRNA.

DR EMBL; X05019; CAA28675.1; -; mRNA.

DR PIR; A29924; A29924.

DR HSSP; Q00955; I0D4.

DR Ensembl; ENSGALG00000005439; Gallus gallus.

DR InterPro; IPR011761; ATP GRASP.

DR InterPro; IPR011764; BC_

DR InterPro; IPR001882; Biotin BS

DR InterPro; IPR005482; Biotin_carb C.

DR InterPro; IPR000089; Biotin_lipoyl.

DR InterPro; IPR000022; Carboxyl trans.

DR InterPro; IPR011763; COA CT C.

DR InterPro; IPR011762; COA CT N.

DR InterPro; IPR005481; Cbase_L N.

DR InterPro; IPR005479; Cbase_D2_ATP_bd.

DR Pfam; PF02785; Biotin carb C; 1.

DR Pfam; PF00364; Biotin lipoyl; 1.

DR Pfam; PF01039; Carboxyl trans; 1.

DR Pfam; PF0289; Cbase_L chain; 1.

DR Pfam; PF02786; Cbase_L_D2; 1.

DR PROSITE; PS00975; ATP_GRASP; 1.

DR PROSITE; PS00979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00968; BIOTINYL LIPOYL; 1.

DR PROSITE; PS00989; COA CT_NTER; 1.

DR PROSITE; PS00980; COA CT_CTER; 1.

DR PROSITE; PS00866; CBASE_1; 1.

DR PROSITE; PS00867; CBASE_2; 1.

KW ATP-binding; Biotin; Direct protein sequencing;

KW Fatty acid biosynthesis; Ligase; Lipid synthesis;

KW Multifunctional enzyme; Nucleotide-binding; Phosphorylation.

FT DOMAIN 117 618 Biotin carboxylation.

FT DOMAIN 275 466 ATP-grasp.

FT DOMAIN 752 818 Biotinyl/lipoyl.

FT DOMAIN 1675 2171 Carboxyltransferase.

FT NP_BIND 315 320 ATP (Potential).

FT ACT_SITE 441 441 Biotin (covalent).

FT BINDING 786 786 Coenzyme A (By similarity).

FT BINDING 1800 1800 Coenzyme A (By similarity).

FT BINDING 2104 2104 Coenzyme A (By similarity).

FT BINDING 2106 2106 Phosphoserine (By similarity).

FT MOD_RES 78 78 Phosphoserine (By similarity).

FT MOD_RES 80 80 Phosphoserine (By similarity).

FT MOD_RES 1193 1193 Phosphoserine (By similarity).

SQ SEQUENCE 2324 AA; 262720 MW; 3FIC541F01BBEF6 CRC64;

Query Match. 61.2%; Score 1780; DB 1; Length 2324;

Best Local Similarity 63.4%; Pred. No. 3.4e-112;

Matches 343; Conservative 81; Mismatches 103; Indels 14; Gaps 5;

Qy 22 ASPVADPIKGGHSHVTKVLCNNGIAAVKEIRSKWAVETFGDRAIEFTVMATPED 81

Db 103 ASP-AEFTVTFGGRVIEKVLIANNGIAAVKMSIRKSWSTEMFRNRAIRFVVMVTPE 161

Qy 82 LKVNADYIRVADQVEVPGGNNNNVANVDLIVDAERAGVHVAWAGHASENPRLPES 141

Db 162 LKNAEYIKWADHYVPVPGGNNNNVANVELLDIAKIPVQAVWAGHASENPKLP 221

Qy 142 LAASKHKIIFIGPGSAMRSLGDKISSTIVQAHDVPCMPWSGTGKIKETMSD---OGFL 198

Db 222 L--HKGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNGSLRVDMQENDLQKRL 279

Qy 199 TVSDDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGGKIRKCTNGEBFKQLYNVIG 258

Db 280 NVQELYEKGYVDADDGLRAAEVGYPMIKASEGGGGKIRKVNADDFPNLFQVQA 339

Qy 259 EVFGSPVFMKLAGQARHLEVQLADQYGNASIFGRDCSVQRHOKIIEEAPVTIAPED 318

Db 340 EVFGSPVFMRLAKQSHLEVLADQYGNASIFGRDCSVQRHOKIIEEAPASIVTSV 399

Qy 319 ARSMEKAARVLAKLVGVYSAGTVEMLYSPSESEFAFLELNPRLOVHEPHTTEMVGNIP 378

Db 400 VFEHMEQCAVKLAKMVGYSAGTVELYLS-QDGSFYFLELNPRLOVHEPHTTEMVADNLP 458

Qy 379 AAQLQVAMGIPLYSIRDIRTLGYMDPRGNEVIDDFSSPESFKTORQPOGHVACRIT 438

Db 459 AAQLQIAMGIPLHKIKDIRVMYGVSPMGDGSIDFNSA-----HVPCPRGHVIAKIT 511

Qy 439 AENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498

Db 512 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSAAGLHEFADSQFGHCFSGWENREAI 571

Qy 499 KQWVISLKLISIRGDFRTTVEYLIKLETDAPFSNKITKTGWLGLDGLIQRLETAERPPADLA 558

Db 572 SNMVVALKELISIRGDFRTTVEYLIKLETESFQONRIDTGWLDRLIAEKVQAEPRPTMLG 631

Qy 559 V 559

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Db      632 V 632

RESULT 29
Q9V347 DROME PRELIMINARY; PRT; 2482 AA.
AC      Q9V347;
DT      01-MAY-2000 (TRENBLrel. 13, Created)
DT      01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE      CG11198-PA, isoform A.
GN      Name=CG11198; ORFNames=CG11198;
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA      Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA      Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      The genome sequence of Drosophila melanogaster.;
RN      Science 287:2185-2195(2000).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22426065; PubMed=12537568;
RA      Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA      Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA      George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA      Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA      Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA      Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT      "finishing a whole-genome shotgun: release 3 of the Drosophila
RT      melanogaster euchromatic genome sequence.";
RN      Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22426070; PubMed=12537573;
RA      Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Svirskas R.,
RA      Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA      George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA      Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA      Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA      Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT      "finishing a whole-genome shotgun: release 3 of the Drosophila
RT      melanogaster euchromatic genome sequence.";
RN      Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22426069; PubMed=12537572;
RA      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA      Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA      Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA      Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA      Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA      Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA      Lewis S.E.;
RT      "Annotation of the Drosophila melanogaster euchromatic genome: a
RT      systematic review.";
RN      Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RX      Berkeley Drosophila Genome Project;
RA      Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA      Hoskins R., Stapleton M., Paclele J., Park S., Svirskas R., Smith E.,
RA      Yu C., Rubin G.;
RT      "Drosophila melanogaster release 4 sequence.";
RN      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [6]
RP      NUCLEOTIDE SEQUENCE.
RX      Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RA      EMBL; AE003839; AAF59155.2; -; Genomic_DNA.
RA      HSP; Q00955; IOD4.
RA      GO; GO:0005524; F:ATP binding; IEA.
RA      GO; GO:0009374; F:biotin binding; IEA.
RA      GO; GO:0016874; F:ligase activity; IEA.
RA      GO; GO:0008152; P:metabolism; IEA.
RA      InterPro; IPR011761; ATP GRASP.
RA      InterPro; IPR011764; BC.
RA      InterPro; IPR001882; Biotin BS.
RA      InterPro; IPR005482; Biotin carb C.
RA      InterPro; IPR000089; Biotin_lipoyl.
RA      InterPro; IPR000022; Carboxyl_trans.
RA      InterPro; IPR011763; COA CT C.
RA      InterPro; IPR005481; CPase L N.
RA      InterPro; IPR001762; COA CT N.
RA      InterPro; IPR005479; CPase D2 ATP_bd.
RA      Pfam; PF02785; Biotin_carb_C; 1.
RA      Pfam; PF00364; Biotin_lipoyl; 1.
RA      Pfam; PF01039; Carboxyl_trans; 1.
RA      Pfam; PF00289; CPase_L_chain; 1.
RA      Pfam; PF02786; CPase_L_D2; 1.
RA      PROSITE; PS00975; ATP_GRASP; 1.
RA      PROSITE; PS00979; BC; 1.
RA      PROSITE; PS00188; BIOTIN; 1.
RA      PROSITE; PS00968; BIOTINYL_LIPOYL; 1.
RA      PROSITE; PS00989; COA CT CTER; 1.
RA      PROSITE; PS00980; COA CT NTER; 1.
RA      PROSITE; PS00866; CPASE_1; UNKNOWN 1.
RA      PROSITE; PS00867; CPASE_2; UNKNOWN 1.
SQ      SEQUENCE 2482 AA; 278596 MW; F0E6D2B15C676A4C CRC64;

Query Match 61.2%; Score 1780; DB 2; Length 2482.
Best Local Similarity 64.2%; Pred. No. 3.7e-112;
Matches 342; Conservative 69; Mismatches 110; Indels 12; Gaps 4;

Qy      27 DFTKGGHSHVTKVLCNNGIAAVKEIRKWAYETFGDERAIEFTVWATPDLKNA 86
Db      249 EFVKRFGGTRVINKVLINNGIAAVKCRSIRRWAYEMFKRAIRFVVMVTPDLKANA 308
Qy      87 DYIRMDQVVEVPGSGNNNNYNDVLIVDAERAGVHAWAGHASENRPESLAASK 146

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Db 309 EYIKWADHYVPVPGSGNNNNYANVELIIVDIALRTQVAVWAGHASENPKLPELL--HK 366
Qy 147 HKLIPFGPGSMRSLGDKISTIVAHADVPMPWSTGKIKETWMSDQGFVTVSDDDVYQ 206
Db 367 EGLVFLGPPERAMWALGDKVASSIVAOAETPTLPWSGSLDKAQYSGKK--IKISSEIFA 424
Qy 207 QACIHTAEBGLEKAEKIGYPVMIKASGGGGKIRKCTNGBEFKOLYNALVGEVPGSPVF 266
Db 425 RGCVTNVEQGLAANVKIGFPVMIKASGGGGKIRRVDTTTEFPGLFRQVQAEVPGSPIF 484
Qy 267 VMKLAGARHLEVLQADDOYGNASIFORDCSVORRHQKIIEEAPVTIAPEDAREMEKA 326
Db 485 VMKLAGARHLEVLQADDOYGNASIFORDCSVORRHQKIIEEAPVIAQAEVFEDEMEKA 544
Qy 327 AVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPHPTTEMVSGVNIIPAQLQVAM 386
Db 545 AVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPHPTTEMVSGVNIIPAQLQVAM 603
Qy 387 GIPLYRSLRDLTYGMDPRGNEVIDDFSSPESFKTORQPOGHVAVACRITAENPDPTGF 446
Db 604 GIPLYRSLRDLTYGMDPRGNEVIDDFSSPESFKTORQPOGHVAVACRITAENPDPTGF 656
Qy 447 KPGMGALTELNRSTSTWGYFSGVTSGALHEYADSFQGHIFAYGADRSEARKQWISLK 506
Db 657 KPSSGTQVQLNFRSSKNVWGYFSAAGSLGHEFADSFQGHIFAYGADRSEARKQWISLK 716
Qy 507 ELSIRGDPRTTVEYLIKLETDAPESNKITTCGLDGLIQLDRLTAERPPADLAV 559
Db 717 ELSIRGDPRTTVEYLIKLETDAPESNKITTCGLDGLIQLDRLTAERPPADLAV 769

RESULT 30
Q6JIZ1_MOUSE PRELIMINARY; PRT; 2345 AA.
ID Q6JIZ1_MOUSE PRELIMINARY; PRT; 2345 AA.
AC Q6JIZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Acetyl-CoA carboxylase 1.
GN Name=Acaca; Synonyms=Acac;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Mao J., Wakil S.J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451393; AAS13685.1; -, mRNA.
DR MGI; MGI:108451; Acaca.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IMP.
DR InterPro; IPR011761; ATP GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT_C.
DR InterPro; IPR011762; COA CT_N.
DR InterPro; IPR005481; Phase_I_N.
DR InterPro; IPR005479; Phase_D2_ATP_bd.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS09075; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS09068; BIOTINYL_LIPOYL; 1.
DR PROSITE; PS09089; COA_CT_CTER; 1.

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DR PROSITE; PS09080; COA_CT_NTER; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
SQ SEQUENCE 2345 AA; 265121 MW; D483B4CECCF6C7D8 CRC64;

Query Match 61.1%; Score 1776; DB 2; Length 2345;
Best Local Similarity 63.4%; Pred. No. 6.4e-112;
Matches 343; Conservative 79; Mismatches 105; Indels 14; Gaps 5;

Qy 22 ASPVADPIRKGQSHVITKVLICNNGIAAATKIRKWAYETPGDRAIEFTVMAITPD 81
Db 102 ASP-AEFTVTRFGNKVIEKVLIANNGIAAATKIRKWAYETPGDRAIEFTVMAITPD 160
Qy 82 LKNADYIRNADQVVEVPGSGNNNNYANVELIIVDVAERAGVHVAWAGHASENPRLPES 141
Db 161 LKANAEYIKWADHYVPVPGSGNNNNYANVELIIVDVAERAGVHVAWAGHASENPRLPES 220
Qy 142 LAASKKIKIIFIGPPGSMRSLGDKISTIVAHADVPMPWSTGKIKETWMSD---QGFL 198
Db 221 LL--KNGIAFMGPPSQAMWALGDKIASSIVAOAETPTLPWSGSLRVDNQENDFSKRIL 278
Qy 199 TVSDDDVYQACIHTAEBGLEKAEKIGYPVMIKASGGGGKIRKCTNGBEFKOLYNALV 258
Db 279 NVPDQLEYKGVVDVDDGLKAAEBEGVPMIKASGGGGKIRKCTNGBEFKOLYNALV 338
Qy 259 EVPGSPVFMKLAGARHLEVLQADDOYGNASIFORDCSVORRHQKIIEEAPVTIAPED 318
Db 339 EVPGSPVFMKLAGARHLEVLQADDOYGNASIFORDCSVORRHQKIIEEAPVTIAPED 398
Qy 319 ARPSMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPHPTTEMVSGVNI 378
Db 399 VFEHMEQCAVRLAKLVGYVSAGTVEWLYSPESGEFAPLELNPRLQVEHPHPTTEMVSGVNI 457
Qy 379 AQLQVAMGIPLYSIRDIRTYLGMNPRGNEVIDDFSSPESFKTORQPOGHVAVACRIT 438
Db 458 AQLQVAMGIPLYSIRDIRTYLGMNPRGNEVIDDFSSPESFKTORQPOGHVAVACRIT 510
Qy 439 AENPDPTGFKPGMGALTELNRSTSTWGYFSGVTSGALHEYADSFQGHIFAYGADRSEAR 498
Db 511 SENPDPTGFKPGMGALTELNRSTSTWGYFSGVTSGALHEYADSFQGHIFAYGADRSEAR 570
Qy 499 KQWISIKELSIKIRGDPRTTVEYLIKLETDAPESNKITTCGLDGLIQLDRLTAERPPADLA 558
Db 571 SNNVVALKELSIKIRGDPRTTVEYLIKLETDAPESNKITTCGLDGLIQLDRLTAERPPADLA 630
Qy 559 V 559
Db 631 V 631

RESULT 31
COAL_BOVIN STANDARD; PRT; 2346 AA.
ID COAL_BOVIN STANDARD; PRT; 2346 AA.
AC Q9TTS3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin
DE carboxylase (EC 6.3.4.14)].
GN Name=ACACA; Synonyms=ACAC, ACCA;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21378179; PubMed=11485560; DOI=10.1042/0264-6021:3580127;
RA Mao J., Marcos S., Davis S.K., Burzlaff J., Seyfert H.-W.;
RT "Genomic distribution of three promoters of the bovine gene encoding
RT acetyl-CoA carboxylase alpha and evidence that the nutritionally
RT regulated promoter I contains a repressive element different from that

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DR	InterPro	IPR011761	ATP GRASP	Query Match	60.9%	Score 1769.5	DB 2	Length 2458
DR	InterPro	IPR011764	BC	Best Local Similarity	63.4%	Pred. No. 1.9e-111		
DR	InterPro	IPR005482	Biotin carb C	Matches 34	Conservative 75	Mismatches 107	Indels 17	Gaps 7
DR	InterPro	IPR000089	Biotin_lipo1					
DR	InterPro	IPR000022	Carboxyl trans					
DR	InterPro	IPR011763	COA CT C					
DR	InterPro	IPR011762	COA CT N					
DR	InterPro	IPR005481	Cpase L N					
DR	InterPro	IPR005479	Cphp synth L D2					
DR	InterPro	IPR002114	Hpr Serp S					
DR	Pfam	PF02785	Biotin carb C					
DR	Pfam	PF00364	Biotin_lipo1					
DR	Pfam	PF01039	Carboxyl trans					
DR	Pfam	PF00289	Cpase L chain					
DR	Pfam	PF02786	Cpase L D2					
DR	PROSITE	PS50975	ATP GRASP					
DR	PROSITE	PS50973	BC					
DR	PROSITE	PS50968	BIOTINYL LIPOYL					
DR	PROSITE	PS50989	COA CT CTER					
DR	PROSITE	PS50980	COA CT NTER					
DR	PROSITE	PS00866	CPSASE_1					
DR	PROSITE	PS00867	CPSASE_2					
DR	PROSITE	PS00589	PTS_HPR_SER					
KW	Ligase							
SQ	SEQUENCE	2458 AA	276553 MW	E9E072A910B490A5	CRC64			
Qy	22	ASPVADPIRQGGHSHVTKVLICNNGIAA	AKVEIRSKWAYETTFQDERAIEFTVMATPD	81				
Db	245	ASP-ABFVTRFGDVRVIEKVL	IANNGIAA	VKMSIREWAYEMFRNERAIRFVMVTPD	303			
Qy	82	LKNVADYIRMAQDYVEYFGSSNNNNYANVD	LIVDAERAGVHAVWAGHGHA	SENPRLPBS	141			
Db	304	LKANAERYIKMADHYVPYFGGPNNNNYANVEL	IVDIKRIPIQVAVWAGHGHA	SENKLPCL	363			
Qy	142	LAASKHKIIIFIGPPGSAMRSLGDKI	ISTTIVAQHADVPCMPWSGTG	IKETWMSD--QG-F	197			
Db	364	LC--KNGVAFLGPPSEAWALGD	KIATSTVVAQTLOVFTLPWSGSL	TVTEWDEDDLQOQKR	421			
Qy	198	LTVSDDDYQQA	CIHTAEGLKAEKIGYPVMIKAS	EGGGGKIRKCTNGEEFKQLYNVL	257			
Db	422	ISVPEDYVYD	KGCVKVDVDEGLEAAERIGFPLMIK	ASGGGGKIRKASAEADFPILFRQVQ	481			
Qy	258	GEVPGSPVFMV	KLGAQARHLEVLADQYAGNAIS	IFQDSCVQRHQKIIIEAPVTIAPE	317			
Db	482	SETPGSPIFLM	KLGAQARHLEVLADQYAGNAIS	IFQDSCVQRHQKIIIEAPVTIAPE	541			
Qy	318	DARESMEKAVRLAKL	GVYVSAGVTEWLYSPESGEFA	FLNPLRLOVEHPTTEMVGYNI	377			
Db	542	AIPEFMEQCAIRLAKT	GVYVSAGVTEWLYS-QDGSF	HLELNPLRLOVEHPTTEMVADYNL	600			
Qy	378	PAAQLOVAMGI	PIYSIRDIITLYGMDPRGNEVID	DFDSSPESFKT-QRKPOQGHVACR	436			
Db	601	PAAQLOVAMG	VLRLKDXIRLLYGESEWG-----	VTPISFETSPNPPLARGHVIAR	652			
Qy	437	ITANPDTPGPK	PGMGALTELNFRSSSTWGYFS	VGTSFSGALHEYADSQGHIFAYGADSE	496			
Db	653	ITSENDEGFKP	SSGTVOELNFRSSKNWGYFS	VAAATGGLHEFADSQGHCFSGWENREE	712			
Qy	497	ARKQWISL	KELSRIGDFRTTVEYLLIKL	ETDAFESNKITTGWLDGLIQDLTAERP	556			
Db	713	AISNMVVAL	KELSRIGDFRTTVEYLLINL	LETESFQNNIDITGWLIDLYIAEKVQAEKPDIM	772			
Qy	557	LAV	559					
Db	773	LGV	775					

RESULT 35

06TY48 HUMAN

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ID AC Q6TY48_HUMAN PRELIMINARY; PRT; 2458 AA.
DI Q6TY48_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Acetyl-CoA carboxylase 2 (EC 6.4.1.2).
GN Name=ACC2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue:Heart;
RA Mao J., Wakil S.J.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL AY382667; AAR37018.1; -, mRNA.
DR GO; GO:0009343; C:biotin carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC_CT_N.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000889; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT C.
DR InterPro; IPR011762; COA CT N.
DR InterPro; IPR005481; CPase L_N.
DR InterPro; IPR005479; Cphp_synth_L_D2.
DR InterPro; IPR002114; HPr_Serp_S.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00284; CPase L_chain; 1.
DR Pfam; PF02786; CPase L_D2; 1.
DR PROSITE; PS00975; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS00989; COA CT CTER; 1.
DR PROSITE; PS00980; COA CT NTER; 1.
DR PROSITE; PS00866; CPASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 2458 AA; 276539 MW; 08C54086D5B2DC16 CRC64;

Query Match 60.9%; Score 1769.5; DB 2; Length 2458;
Best Local Similarity 63.5%; Pred. No. 1.9e-111;
Matches 345; Conservative 73; Mismatches 108; Indels 17; Gaps 7;

QY 22 ASPVADFTKGGHGVITKVLICNGGIAAKVIRKWAYTFGDERAIEFTVMATPE 81
DB 245 ASP-AEFTVRFGGDVIKVLVANGIAAKVIRKWAYEMFNERAIRFVVMVTE 303

QY 82 LKVNADYIRMDQYVEVFGSGNNNNYANVDLIVDAERAGHAVWAGHGHASEN 141
DB 304 LKANAAYIKMADHYVPVPGPNNNYANVELIVDAIRKIPQAVWAGHGHASEN 363

QY 142 LAASKHKIPIFGPSAMRSLGDKISSTIVAGHADVPCMPWSGTGKETMMSD--- 198
DB 364 LC--KNGVAFLGPPSEAMWALGDKIASTVTAQTLVPTLPWSSGLTVEWTE 421

QY 199 T-VSDVVOQACIHTAEGLKAEKIGYPMVKASGGGKIGKCTNGEREKQLYNAVL 257
DB 422 TSPVSDVVDKGVCKVDVEGLAEARIGFPLMKASGGGKIGIRKAEASGDPILFR 481

QY 258 GSVPGSPVFMKLAGQARHLEVQLLADQYGNATISIFGRDCSVQRHOKIIEAP 317
DB 482 SEIPGSPFLMKLAGQARHLEVQLLADQYGNATISIFGRDCSVQRHOKIIEAP 541

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RESULT 36

Q7PQ11 ANOGA

ID Q7PQ11 ANOGA PRELIMINARY; PRT; 2314 AA.

AC Q7PQ11;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE ENSANGP00000015662 (Fragment).

GN ORFNames=ENSANGG00000013173;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;

OC Anophelinae; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN-PEST;

RG The Anopheles gambiae Sequence Committee;

RT "Anopheles gambiae re-annotation.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN-PEST;

RG The Anopheles gambiae Sequence Committee;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAB01008900; EAA09449.3; -; Genomic_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0009374; F:biotin binding; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR011761; ATP_GRASP.

DR InterPro; IPR011764; BC_CT_N.

DR InterPro; IPR001882; Biotin BS.

DR InterPro; IPR005482; Biotin carb C.

DR InterPro; IPR000089; Biotin lipoyl.

DR InterPro; IPR000022; Carboxyl trans.

DR InterPro; IPR011763; COA CT C.

DR InterPro; IPR011762; COA CT_N.

DR InterPro; IPR005481; CPase L_N.

DR InterPro; IPR005479; Cphp_synth_L_D2.

DR Pfam; PF02785; Biotin carb C; 1.

DR Pfam; PF00364; Biotin lipoyl; 1.

DR Pfam; PF01039; Carboxyl trans; 1.

DR Pfam; PF00289; CPase L_chain; 1.

DR Pfam; PF02786; CPase L_D2; 1.

DR PROSITE; PS00975; ATP_GRASP; 1.

DR PROSITE; PS00979; BC; 1.

DR PROSITE; PS00188; BIOTIN; 1.


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QY 265 VEVNKLAGQARHLEVOALLADQYNAISIFGRDCSVORRHOKIIEEAPVTIAPEDARESME 324
Db 241 IFFMVLVSNKHLSEVQIVADRHGAISLNGRDCSVORRHOKIIEEGPAIAPTQVWEEME 300
QY 325 KAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIIPAAQLQV 384
Db 301 RAAVRLKVEGVGAGTVEYLFA--EGEYFLELNPRLOVEHPVTEQITGVNLPATQLQI 358
QY 385 AMGIPLYSIRDIRTYLGM---DPRGNEVIDF-DSSSPESFKTQKPOQGHVACRITAE 440
Db 359 AMGIPLHRIIPDIRKLYGRTGDDLYGDSMIDLHDF-----TKENP-PAGHCIAVRITGE 410
QY 441 NPDTGFPGMGALTELNFRSSTSTWGYFVSCTGALHEYADSOFGHIFAYGADRSEARKQ 500
Db 411 NPDEGFPTSGQIHLELFRSTPNWGYFVSQAKGLHEYADSOFGHIFANGATREARKT 470
QY 501 MVISKELSGIRGDRFTTVEYLKLELTDAPESNKITTGWLDDGLIQRDLTAERPDLAV 559
Db 471 IILGKLSIRGDIRTPVEYIIHLESKDFKENIHTGWLDDGLISEKIQTKKPETMIVV 529

RESULT 40
O70151 RAT
ID O70151 RAT PRELIMINARY; PRT; 2456 AA.
AC O70151
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyl-CoA carboxylase.
GN Name=Acacb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar;
RX MEDLINE=98322122; PubMed=9655932; DOI=10.1016/S0167-4781(98)00060-8;
RA Abe K., Shinohara Y., Terada H.;
RT "Isolation and characterization of cDNA encoding rat muscle type
RL Biochim. Biophys. Acta 1398:347-352 (1998).
DR EMBL; AB004329; BAA25799.1; -; mRNA.
DR HSSP; Q00955; 10D4.
DR Ensembl; ENSRNOG00000000658; Rattus norvegicus.
DR RGD; 620500; Acacb.
DR GO; GO:0009343; C:biotin carboxylase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004075; F:biotin carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011761; ATP_GRASP.
DR InterPro; IPR011764; BC.
DR InterPro; IPR005482; Biotin carb. C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000022; Carboxyl trans.
DR InterPro; IPR011763; COA CT C.
DR InterPro; IPR011762; COA CT N.
DR InterPro; IPR005481; CPhase_L_N.
DR InterPro; IPR005479; Cphph_synth_L_D2.
DR InterPro; IPR002114; HPr_Serp_S.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF01039; Carboxyl trans; 1.
DR Pfam; PF00289; CPhase_L_chain; 1.
DR Pfam; PF02786; CPhase_L_D2; 1.
DR PROSITE; PS00975; ATP_GRASP; 1.
DR PROSITE; PS00979; BC; 1.
DR PROSITE; PS00968; BIOTINYL LIPOYL; 1.
DR PROSITE; PS00989; COA CT CTER; 1.
DR PROSITE; PS00980; COA CT NTER; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.

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DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR PROSITE; PS00589; PTS_HPE_SER; UNKNOWN_1.
SQ SEQUENCE 2456 AA; 276098 MW; CUD41AF0BEA38863 CRC64;

Query Match 57.6%; Score 1673.5; DB 2; Length 2456;
Best Local Similarity 60.2%; Pred. No. 6.9e-105;
Matches 327; Conservative 78; Mismatches 121; Indels 17; Gaps 7;

QY 22 ASPVADPIRKGQGHSHVITKVLNNGNIAAIVKRSIRKWAYETFGDERATEFTVMATPED 81
Db 241 ASP-AEFVTRFGGNRIETVLIANNGIAAVKWRISRRWAYEMFRNERAIRFVVMVTPED 299
QY 82 LKNADYIRMAQDYVEVPGSGNNNNYANVDLIYDVAERAGVAVWAGHGHASENPLRPES 141
Db 300 LKANAEYYKADVLVPVPGGPNNNYANVELIIDIAKRIPVQAVWAGHGHASENPKLP 359
QY 142 LAASKHKIIFIGPPGSAIRSLGDKISSTIVAQHADVPKMPWSGTGKETMMSD---QG-F 197
Db 360 LC--KHGIAFLGPRVRPMLGLGDRLSSTIVAQTLQIPTLPWSGSLTVEWTEDSQHGGK 417
QY 198 LTVSDVYQACIHTAEBGLEKAKKIGYPVMIKASGGGGKGIKCTNGBEFKQLYNVL 257
Db 418 ISVTEDVYEQGVDRDVEGLQAAEKVGFPLMIKASEGGGGKGIROAESADFPFCFRQV 477
QY 258 GEVPGSPVFMKLAGOARHLEVOALLADQYNAISIFGRDCSVORRHOKIIEEAPVTIAP 317
Db 478 SEIPGSPFIMKLAQARHLEVOALLADQYNAISIFGRDCSVORRHOKIIEEAPVTIAP 537
QY 318 DARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGNI 377
Db 538 AVFEFMEQCAVLLAKTVVVSAGTVGLYS-QDGSFHFLELNPRLOVEHPTTEMVSGNI 596
QY 378 PAAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTQKPO-QGHVACR 436
Db 597 PAAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTQKPO-QGHVACR 648
QY 437 ITAENPDITGKPGMGALTELNFRSSTSTWGYFVSCTGALHEYADSOFGHIFAYGADRSE 496
Db 649 ITSNDPEAFKPSGGVQELNFRSNVWGYFVSVAAGGLHEFPISQFGHCFSENGEQEE 708
QY 497 ARKQMVISLKELSGIRGDRFTTVEYLKLELTDAPESNKITTGWLDDGLIQRDLTAERP 556
Db 709 AISNMVVALKELSGIRGDRFTTVEYLKLELTDAPESNKITTGWLDDGLIQRDLTAERP 768
QY 557 LAV 559
Db 769 LGV 771

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Search completed: February 4, 2006, 18:12:51
Job time : 253 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:25:06 ; Search time 183 Seconds

(without alignments)
1276.320 Million cell updates/sec

Title: US-10-633-835-2

Perfect score: 2907

Sequence: 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDLRTAERPADLAV 559

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2907	100.0	559	4	US-10-633-835-2
2	2885	99.2	554	4	US-10-633-835-22
3	2881	99.1	554	4	US-10-633-835-27
4	2872	98.8	554	4	US-10-633-835-17
5	2857	98.3	549	4	US-10-633-835-23
6	2850	98.0	549	4	US-10-633-835-18
7	2850	98.0	549	4	US-10-633-835-24
8	2808	96.6	539	4	US-10-633-835-28
9	2800	96.3	539	4	US-10-633-835-29
10	2797	96.2	539	4	US-10-633-835-19
11	2751	94.6	529	4	US-10-633-835-25
12	2747	94.5	529	4	US-10-633-835-30
13	2746	94.5	529	4	US-10-633-835-20
14	2703	93.0	519	4	US-10-633-835-26
15	2698	92.8	519	4	US-10-633-835-31
16	2694	92.7	519	4	US-10-633-835-21
17	2163	74.4	571	4	US-10-633-835-53
18	2163	74.4	581	4	US-10-633-835-52
19	2163	74.4	591	4	US-10-633-835-6
20	2139	73.6	2301	4	US-10-369-493-3698
21	2135	73.5	581	4	US-10-633-835-54
22	2109	72.5	571	4	US-10-633-835-55
23	2079.5	71.5	2241	4	US-10-369-493-2130
24	2074	71.3	521	4	US-10-633-835-64
25	2060	70.9	560	4	US-10-633-835-35
26	2060	70.9	570	4	US-10-633-835-34
27	2060	70.9	575	4	US-10-633-835-33

ALIGNMENTS

RESULT 1

US-10-633-835-2

; Sequence 2, Application US/10633835

; Publication No. US20040086994A1

; GENERAL INFORMATION:

; APPLICANT: Elich, Tedd D.

; APPLICANT: Weatherly, Stephanie C.

; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF

; FILE REFERENCE: 9280.2

; CURRENT APPLICATION NUMBER: US/10/633,835

; PRIOR FILING DATE: 2003-08-04

; PRIOR FILING DATE: 2003-08-05

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 2

; LENGTH: 559

; TYPE: PRT

; ORGANISM: Ustilago maydis

US-10-633-835-2

Query Match 100.0%; Score 2907; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 3e-254;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	PPPDHKAVSQFIGGNPLETAPAPSPVADFIKQGHSHVITKVLICNNGIAAVKEIRSIRKW	60
Db	1	PPPDHKAVSQFIGGNPLETAPAPSPVADFIKQGHSHVITKVLICNNGIAAVKEIRSIRKW	60
Qy	61	AYETFGDERAIEFTVWATPDLKVNADYIRMDQYVEVPGSGNNNNYANDVLIYDVARA	120
Db	61	AYETFGDERAIEFTVWATPDLKVNADYIRMDQYVEVPGSGNNNNYANDVLIYDVARA	120
Qy	121	GVHAWAGHGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAOHADVPCM	180
Db	121	GVHAWAGHGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAOHADVPCM	180
Qy	181	PWSGTGKETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVWKASEGGGKGI	240
Db	181	PWSGTGKETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVWKASEGGGKGI	240
Qy	241	RKCTNGEEFKQLNVLGVPGSPVFMKLAGARHLEVQLLADQYGNNAISIFGRDCSVQ	300
Db	241	RKCTNGEEFKQLNVLGVPGSPVFMKLAGARHLEVQLLADQYGNNAISIFGRDCSVQ	300
Qy	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTVWLYSPESGEFAFLELNP	360
Db	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGVVSAGTVWLYSPESGEFAFLELNP	360

Qy 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
Db 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
Qy 421 KTORPQPOGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGYSVGTSGALHEYA 480
Db 421 KTORPQPOGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGYSVGTSGALHEYA 480
Qy 481 DSQFGHIFAYGADRSEARKQWISLKELSGIRGDFRTTVEYLKLETDAFESNKITTGWL 540
Db 481 DSQFGHIFAYGADRSEARKQWISLKELSGIRGDFRTTVEYLKLETDAFESNKITTGWL 540
Qy 541 DGLIQDLRLTAERPPADLAV 559
Db 541 DGLIQDLRLTAERPPADLAV 559

RESULT 2

US-10-633-835-22
; Sequence 22, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(554)
; OTHER INFORMATION: C-terminal deleted Ustilago Accase BC domain (AAs 2-555)
US-10-633-835-22

Query Match 99.2%; Score 2885; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.9e-252;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVTKVLICNNGIAA VKEIRSKW 60
Db 1 PPPDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVTKVLICNNGIAA VKEIRSKW 60
Qy 61 AVETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERA 120
Db 61 AVETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERA 120
Qy 121 GVHAWAGGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
Db 121 GVHAWAGGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
Qy 181 PWSGTGKETMMSDQGFITVSDVYQACIHTAEBGLEKAEKIGYPVMIKASEGGGKGI 240
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Qy 241 RKTNGEEFKOLYNALVGEVPGSPVFMKLAGOARHLEVOLLADQYGNALISIFGRDCSVQ 300
Db 241 RKTNGEEFKOLYNALVGEVPGSPVFMKLAGOARHLEVOLLADQYGNALISIFGRDCSVQ 300
Qy 301 RRHOKIIEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNP 360
Db 301 RRHOKIIEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNP 360

Qy 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
Db 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
Qy 421 KTORPQPOGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGYSVGTSGALHEYA 480
Db 421 KTORPQPOGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGYSVGTSGALHEYA 480
Qy 481 DSQFGHIFAYGADRSEARKQWISLKELSGIRGDFRTTVEYLKLETDAFESNKITTGWL 540
Db 481 DSQFGHIFAYGADRSEARKQWISLKELSGIRGDFRTTVEYLKLETDAFESNKITTGWL 540
Qy 541 DGLIQDLRLTAERPP 554
Db 541 DGLIQDLRLTAERPP 554
RESULT 3
US-10-633-835-27
; Sequence 27, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL CoA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(554)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago Accase BC domain (AAs 4-547)
US-10-633-835-27

Query Match 99.1%; Score 2881; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 6.8e-252;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHSHVTKVLICNNGIAA VKEIRSKW 62
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Qy 63 ETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERAGV 122
Db 61 ETFGDERAIEFTVMATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERAGV 120
Qy 123 HAVWAGGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCWP 182
Db 121 HAVWAGGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCWP 180
Qy 183 SGTGKETMMSDQGFITVSDVYQACIHTAEBGLEKAEKIGYPVMIKASEGGGKGI 242
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Db 241 CTNGEEFKOLYNALVGEVPGSPVFMKLAGOARHLEVOLLADQYGNALISIFGRDCSVOR 300
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Db 301 HQKIIEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNPRL 360
Qy 363 QVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 422

Db 361 QVEHPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQK 420
Qy 423 ORKPOQHVVACRITAENPDGFKPGMGALTELNFPSSTSTWGVFSGTSGALHEYADSFG 482
Db 421 ORKPOQHVVACRITAENPDGFKPGMGALTELNFPSSTSTWGVFSGTSGALHEYADSFG 480
Qy 483 QFGHIFAYGADRSEARKQWISLKELSRGDFRTTVEYLKLETDAPESNKITTTGWLDDG 542
Db 481 QFGHIFAYGADRSEARKQWISLKELSRGDFRTTVEYLKLETDAPESNKITTTGWLDDG 540
Qy 543 LIQDRLTAERPPAD 556
Db 541 LIQDRLTAERPPAD 554

RESULT 4

US-10-633-835-17
; Sequence 17, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(554)
; OTHER INFORMATION: N-terminal deleted Ustilago Accase BC domain (AAs 7-560)
US-10-633-835-17

Query Match 98.8%; Score 2872; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 4.4e-251;
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 KAVSOFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAA VKEIRKWAYETTF 65
Db 1 KAVSOFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAA VKEIRKWAYETTF 60
Qy 66 GDERAIEFTVMTAPDLKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHAV 125
Db 61 GDERAIEFTVMTAPDLKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHAV 120
Qy 126 WAGWGHASENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSGT 185
Db 121 WAGWGHASENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCMPWSGT 180
Qy 186 GIKETMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 245
Db 181 GIKETMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 240
Qy 246 GEEFKQLYNVLGEVPGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVQRHOK 305
Db 241 GEEFKQLYNVLGEVPGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVQRHOK 300
Qy 306 IIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNPRLQVE 365
Db 301 IIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNPRLQVE 360
Qy 366 HPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQK 425

Db 361 HPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQK 420
Qy 426 POQGHVVACRITAENPDGFKPGMGALTELNFPSSTSTWGVFSGTSGALHEYADSFG 485
Db 421 POQGHVVACRITAENPDGFKPGMGALTELNFPSSTSTWGVFSGTSGALHEYADSFG 480
Qy 486 HIFAYGADRSEARKQWISLKELSRGDFRTTVEYLKLETDAPESNKITTTGWLDDGLIQ 545
Db 481 HIFAYGADRSEARKQWISLKELSRGDFRTTVEYLKLETDAPESNKITTTGWLDDGLIQ 540
Qy 546 DRLTAERPPADLAV 559
Db 541 DRLTAERPPADLAV 554
RESULT 5
US-10-633-835-23
; Sequence 23, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(549)
; OTHER INFORMATION: C-terminal deleted Ustilago Accase BC domain (AAs 2-550)
US-10-633-835-23

Query Match 98.3%; Score 2857; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 1e-249;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPPDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAA VKEIRKWAYETTF 60
Db 1 PPPDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAA VKEIRKWAYETTF 60
Qy 61 AYETFGDERAIEFTVMTAPDLKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERA 120
Db 61 AYETFGDERAIEFTVMTAPDLKVNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERA 120
Qy 121 GVHAWAGWGHASENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCM 180
Db 121 GVHAWAGWGHASENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTTVAQHADVPCM 180
Qy 181 PWSGTGIKETMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 240
Db 181 PWSGTGIKETMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIRKCTN 240
Qy 241 RKCTNGSEFFKQLYNVLGEVPGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVQ 300
Db 241 RKCTNGSEFFKQLYNVLGEVPGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVQ 300
Qy 301 RRHQKIIIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNP 360
Db 301 RRHQKIIIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVEWLYSPSGEFAFLELNP 360
Qy 361 RLQVEHPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420
Db 361 RLQVEHPTTEMVSGVNIPTAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420

Db 421 POQGHVACRITAEKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 480
Qy 486 HIFAYGADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 545
Db 481 HIFAYGADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 540
Qy 546 DRLTAERPP 554
Db 541 DRLTAERPP 549

RESULT 8
US-10-633-835-24
; Sequence 24, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 24
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Ustilago maydis
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(539)
; OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)
US-10-633-835-24

Query Match 96.6%; Score 2808; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.7e-245;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPDHKAQVQIFGNPLETAPSPVADPIRQGGHSHVITKVLICNNGIAAVKEIRSKW 60
Db 1 PPDHKAQVQIFGNPLETAPSPVADPIRQGGHSHVITKVLICNNGIAAVKEIRSKW 60
Qy 61 AYETFGDERATEFTVMTATPELKNADYIRMDQYVEVPGSSNNNNYANVDLI 120
Db 61 AYETFGDERATEFTVMTATPELKNADYIRMDQYVEVPGSSNNNNYANVDLI 120
Qy 121 GVHVAWAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
Db 121 GVHVAWAGWGHASNPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
Qy 181 PWSGTGKETMWSOGFLTVDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGI 240
Db 181 PWSGTGKETMWSOGFLTVDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGI 240
Qy 241 RKTNGEEFKOLYNALGVEPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300
Db 241 RKTNGEEFKOLYNALGVEPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300
Qy 301 RRHQKIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360
Db 301 RRHQKIEEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360
Qy 361 RLQVEHPTTEMVSGVNIAPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420
Db 361 RLQVEHPTTEMVSGVNIAPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESF 420
Qy 421 KTQKPOQGHVACRITAEKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 480

Db 421 KTQKPOQGHVACRITAEKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 480
Qy 481 DSQGHIPAYGADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 539
Db 481 DSQGHIPAYGADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 539
RESULT 9
US-10-633-835-29
; Sequence 29, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 29
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Ustilago maydis
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(539)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550)
US-10-633-835-29

Query Match 96.3%; Score 2800; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.4e-244;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 FIGGNPLETAPSPVADPIRQGGHSHVITKVLICNNGIAAVKEIRSKWYETFGDERA 70
Db 1 FIGGNPLETAPSPVADPIRQGGHSHVITKVLICNNGIAAVKEIRSKWYETFGDERA 60
Qy 71 IEFTVMTATPELKNADYIRMDQYVEVPGSSNNNNYANVDLI 130
Db 61 IEFTVMTATPELKNADYIRMDQYVEVPGSSNNNNYANVDLI 120
Qy 131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCWMSGTGIKET 190
Db 121 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCWMSGTGIKET 180
Qy 191 MMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEEFK 250
Db 181 MMSDQGLTVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEEFK 240
Qy 251 QLYNAVLEGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEA 310
Db 241 QLYNAVLEGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEEA 300
Qy 311 PVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPLOVEHPHTE 370
Db 301 PVTIAPEDARESMKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPLOVEHPHTE 360
Qy 371 MVSQVNIAPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQRKPOQ 430
Db 361 MVSQVNIAPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQRKPOQ 420
Qy 431 HVACRITAEKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 490
Db 421 HVACRITAEKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 480
Qy 491 GADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 549
Db 481 GADRSEARKQVLSKELSGDPRFTTVEYLKLETDAFESNKTITGW 539

RESULT 10
US-10-633-835-19
; Sequence 19, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 539
; TYPE: PRP
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(539)
; OTHER INFORMATION: N-terminal deleted Ustilago Accse BC domain (AAs 22-560)
US-10-633-835-19

Query Match 96.2%; Score 2797; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.7e-244; Mismatches 0; Indels 0; Gaps 0;
Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 PASPVADIRKQGGHSHVITKVLICNNGIAAVERKIRKWAYETFGDERAIEFTWATPE 80
DB 1 PASPVADIRKQGGHSHVITKVLICNNGIAAVERKIRKWAYETFGDERAIEFTWATPE 60
QY 81 DLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLE 140
DB 61 DLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLE 120
QY 141 SLAASKHKIIFIGPGSAMSRLGDKISSTIVAHADVPCMPWSGTGKETMMSDQGLTV 200
DB 121 SLAASKHKIIFIGPGSAMSRLGDKISSTIVAHADVPCMPWSGTGKETMMSDQGLTV 180
QY 201 SDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNALGEV 260
DB 181 SDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNALGEV 240
QY 261 PGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEAPVTIAPEDAR 320
DB 241 PGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQRHOKIIEAPVTIAPEDAR 300
QY 321 ESMKAAVRLAKLVGVVSAGTVEMLYSPESGFALELNPRLQVHEPTTEMVSGVNI 380
DB 301 ESMKAAVRLAKLVGVVSAGTVEMLYSPESGFALELNPRLQVHEPTTEMVSGVNI 360
QY 381 QLVAMGPIYSIRDTILYGMDPGRNEVIDDFSSPESFKTKRQKPOQGHVACRI 440
DB 361 QLVAMGPIYSIRDTILYGMDPGRNEVIDDFSSPESFKTKRQKPOQGHVACRI 420
QY 441 NPDTGFKPMGALTTELNFSSSTSTWGYFVSGTSGALHEYADSFQGHIFAYGADRSEARKQ 500
DB 421 NPDTGFKPMGALTTELNFSSSTSTWGYFVSGTSGALHEYADSFQGHIFAYGADRSEARKQ 480
QY 501 MVISIKELSGDFTTVEYLKLETDAPFESKNITGWLGLIODRLTAEPPLADLAV 559
DB 481 MVISIKELSGDFTTVEYLKLETDAPFESKNITGWLGLIODRLTAEPPLADLAV 539

RESULT 11
US-10-633-835-25
; Sequence 25, Application US/10633835

Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 529
; TYPE: PRP
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(529)
; OTHER INFORMATION: C-terminal deleted Ustilago Accase BC domain (AAs 2-530)
US-10-633-835-25

Query Match 94.6%; Score 2751; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 3.9e-240; Mismatches 0; Indels 0; Gaps 0;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPPDHKAVSQPIGNGPLETAPASPVADIRKQGGHSHVITKVLICNNGIAAVERKIRK 60
DB 1 PPPDHKAVSQPIGNGPLETAPASPVADIRKQGGHSHVITKVLICNNGIAAVERKIRK 60
QY 61 AYETFGDERAIEFTWATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERA 120
DB 61 AYETFGDERAIEFTWATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLIVDAERA 120
QY 121 GVHAVWAGHASENPRLESLAASKHKIIFIGPGSAMSRLGDKISSTIVAHADVPC 180
DB 121 GVHAVWAGHASENPRLESLAASKHKIIFIGPGSAMSRLGDKISSTIVAHADVPC 180
QY 181 PWSGTGKETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240
DB 181 PWSGTGKETMMSDQGLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240
QY 241 RKTNGEEFKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300
DB 241 RKTNGEEFKQLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVQ 300
QY 301 RHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGFALELNP 360
DB 301 RHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGFALELNP 360
QY 361 RLOVEHPTTEMVSGVNI 420
DB 361 RLOVEHPTTEMVSGVNI 420
QY 421 KTORKPOQGHVACRI 480
DB 421 KTORKPOQGHVACRI 480
QY 481 DSQGHIFAYGADRSEARKQ 529
DB 481 DSQGHIFAYGADRSEARKQ 529

RESULT 12
US-10-633-835-30
; Sequence 30, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2
;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; PRIOR APPLICATION NUMBER: US 60/401,170
;; PRIOR FILING DATE: 2003-08-05
;; NUMBER OF SEQ ID NOS: 71

;; SOFTWARE: PatentIn version 3.2
;; LENGTH: 529
;; TYPE: PRT

;; ORGANISM: Ustilago maydis
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(529)

;; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)
US-10-633-835-30

Query Match 94.5%; Score 2747; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 9e-240;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 PLETAPSPVADFIKQGGHSHVITKVLICNNGIAAIVKSIKRWAYETFGDERAIEFTV 75
Db 1 PLETAPSPVADFIKQGGHSHVITKVLICNNGIAAIVKSIKRWAYETFGDERAIEFTV 60

Qy 76 MATPEDLVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASEN 135
Db 61 MATPEDLVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASEN 120

Qy 136 PRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAGHADVPCMPWSGTGKETMMSDQ 195
Db 121 PRLPESLAASKHKIIFIGPPGSMRSLGDKISSTIVAGHADVPCMPWSGTGKETMMSDQ 180

Qy 196 GFLTVDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNA 255
Db 181 GFLTVDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNA 240

Qy 256 VLGEVPGSPVPMKLAGARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEBAPVTIA 315
Db 241 VLGEVPGSPVPMKLAGARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEBAPVTIA 300

Qy 316 PEDARESEKAARLAKLVGVVSAGTVEWLYSPESGEGFAFLELPRLOVEHPTTEMVSGV 375
Db 301 PEDARESEKAARLAKLVGVVSAGTVEWLYSPESGEGFAFLELPRLOVEHPTTEMVSGV 360

Qy 376 NIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDDFSSPESFKTORPOGHVAVAC 435
Db 361 NIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDDFSSPESFKTORPOGHVAVAC 420

Qy 436 RITAENPDTPKPGMGALTELNFSSSTWGYFSGTSGALHEYADSOFGHIFAYGADRS 495
Db 421 RITAENPDTPKPGMGALTELNFSSSTWGYFSGTSGALHEYADSOFGHIFAYGADRS 480

Qy 496 EARKQWVLSKELSGDFTTVEYLIKLETDAPESNKITTTGWLGLI 544
Db 481 EARKQWVLSKELSGDFTTVEYLIKLETDAPESNKITTTGWLGLI 529

RESULT 13
US-10-633-835-20

;; Sequence 20, Application US/10633835
;; Publication No. US20040086994A1
;; GENERAL INFORMATION:

;; APPLICANT: Ellich, Tedd D.
;; APPLICANT: Volrath, Sandra L.

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; PRIOR APPLICATION NUMBER: US 60/401,170
;; PRIOR FILING DATE: 2003-08-05
;; NUMBER OF SEQ ID NOS: 71

;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 20
;; LENGTH: 529
;; TYPE: PRT

;; ORGANISM: Ustilago maydis
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(529)

;; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)
US-10-633-835-20

Query Match 94.5%; Score 2746; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 KQGGHSHVITKVLICNNGIAAIVKSIKRWAYETFGDERAIEFTVMTPELKVNDYIR 90
Db 1 KQGGHSHVITKVLICNNGIAAIVKSIKRWAYETFGDERAIEFTVMTPELKVNDYIR 60

Qy 91 MADQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHKII 150
Db 61 MADQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPESLAASKHKII 120

Qy 151 FIGPPGSMRSLGDKISSTIVAGHADVPCMPWSGTGKETMMSDQGLTVDVYQACI 210
Db 121 FIGPPGSMRSLGDKISSTIVAGHADVPCMPWSGTGKETMMSDQGLTVDVYQACI 180

Qy 211 HTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNAVIGVPGSPVFMKL 270
Db 181 HTAEGLKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNAVIGVPGSPVFMKL 240

Qy 271 AGARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEBAPVTIAPDARESEKAAVRL 330
Db 241 AGARHLEVOLLADQYGNALISIFGRDCSVORRHQKIIIEBAPVTIAPDARESEKAAVRL 300

Qy 331 AKLVGVVSAGTVEWLYSPESGEGFAFLELPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIP 390
Db 301 AKLVGVVSAGTVEWLYSPESGEGFAFLELPRLOVEHPTTEMVSGVNIIPAAQLQVAMGIP 360

Qy 391 YSIRDITLYGMDPRGNEVIDDFSSPESFKTORPOGHVAVACRTAENPDTPGFKPGM 450
Db 361 YSIRDITLYGMDPRGNEVIDDFSSPESFKTORPOGHVAVACRTAENPDTPGFKPGM 420

Qy 451 GALTENLFRSSTWGYFSGTSGALHEYADSOFGHIFAYGADRSKARQWVLSKELSI 510
Db 421 GALTENLFRSSTWGYFSGTSGALHEYADSOFGHIFAYGADRSKARQWVLSKELSI 480

Qy 511 RGDFTTVEYLIKLETDAPESNKITTTGWLGLIQRDLTAERPPADLAV 559
Db 481 RGDFTTVEYLIKLETDAPESNKITTTGWLGLIQRDLTAERPPADLAV 529

RESULT 14
US-10-633-835-26

;; Sequence 26, Application US/10633835
;; Publication No. US20040086994A1
;; GENERAL INFORMATION:

;; APPLICANT: Ellich, Tedd D.
;; APPLICANT: Volrath, Sandra L.

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

;; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
;; FILE REFERENCE: 9280.2

;; CURRENT APPLICATION NUMBER: US/10/633,835
;; CURRENT FILING DATE: 2003-08-04

```
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(519)
; OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs2-520)
US-10-633-835-26

Query Match          93.0%; Score 2703; DB 4; Length 519;
Best Local Similarity 100.0%; Pred. No. 8.5e-236;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPPDHKAVSQPTGCGPLETAPASPVPADPIRKQGGHSHVITKVLICNNGIAAWEKIRSRKW 60
DB 1 PPPDHKAVSQPTGCGPLETAPASPVPADPIRKQGGHSHVITKVLICNNGIAAWEKIRSRKW 60

QY 61 AYETFGDERAIEFTWATPEDLKVADYIRMDQVVEVPGGNNNNYANVDLIVDVAERA 120
DB 61 AYETFGDERAIEFTWATPEDLKVADYIRMDQVVEVPGGNNNNYANVDLIVDVAERA 120

QY 121 GVHAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180
DB 121 GVHAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCM 180

QY 181 PMSGTGKIKETMMSDQGFITVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGI 240
DB 181 PMSGTGKIKETMMSDQGFITVSDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGI 240

QY 241 RKTNGEERFKOLYNALVGEVPGSPVFMKLAGQARHLEVOLLADQYGNASIFGRDCSVQ 300
DB 241 RKTNGEERFKOLYNALVGEVPGSPVFMKLAGQARHLEVOLLADQYGNASIFGRDCSVQ 300

QY 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNP 360
DB 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNP 360

QY 361 RLOVEHPPTMVGNYIPAAQLQVAMGPIYSIRDIRTLYGMDPRGNEVIDFDFSSPSF 420
DB 361 RLOVEHPPTMVGNYIPAAQLQVAMGPIYSIRDIRTLYGMDPRGNEVIDFDFSSPSF 420

QY 421 KTQKRPQGHVACRITAEENPDTGFKPGMGALTENFRSSTSTWGYSVGTSGALHEYA 480
DB 421 KTQKRPQGHVACRITAEENPDTGFKPGMGALTENFRSSTSTWGYSVGTSGALHEYA 480

QY 481 DSQGFHIFAYGADRSEARKQWISLKELSIKELSIKELSIKELSIKELSIKELSIKELSI 519
DB 481 DSQGFHIFAYGADRSEARKQWISLKELSIKELSIKELSIKELSIKELSIKELSIKELSI
```

```
RESULT 15
US-10-633-835-31
; Sequence 31, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; NAME/KEY: MISC_FEATURE
```

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; LOCATION: (1)..(519)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 22-540)
US-10-633-835-31

Query Match          92.8%; Score 2698; DB 4; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.4e-235;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PASPVADPIRKQGGHSHVITKVLICNNGIAAWEKIRSRKWYETFGDERAIEFTWATPE 80
DB 1 PASPVADPIRKQGGHSHVITKVLICNNGIAAWEKIRSRKWYETFGDERAIEFTWATPE 60

QY 81 DLKNADYIRMDQVVEVPGGNNNNYANVDLIVDVAERAGVHAVWAGHASENPRLPE 140
DB 61 DLKNADYIRMDQVVEVPGGNNNNYANVDLIVDVAERAGVHAVWAGHASENPRLPE 120

QY 141 SLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKIKETMMSDQGFITV 200
DB 121 SLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKIKETMMSDQGFITV 180

QY 201 SDDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGBEFKOLYNALGEV 260
DB 181 SDDVYQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGBEFKOLYNALGEV 240

QY 261 PGSPVFMKLAGQARHLEVOLLADQYGNASIFGRDCSVORRHOKIIEEAPVTIAPEDAR 320
DB 241 PGSPVFMKLAGQARHLEVOLLADQYGNASIFGRDCSVORRHOKIIEEAPVTIAPEDAR 300

QY 321 ESMEKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNPRLQVEHPPTMVGNYIPAA 380
DB 301 ESMEKAAVRLAKLVGVVSAGTVEMLYSPESGEFAFLELNPRLQVEHPPTMVGNYIPAA 360

QY 381 QLQVAMGPIYSIRDIRTLYGMDPRGNEVIDFDFSSPSFQTKRQPOGHVACRITAE 440
DB 361 QLQVAMGPIYSIRDIRTLYGMDPRGNEVIDFDFSSPSFQTKRQPOGHVACRITAE 420

QY 441 NPDTGFKPGMGALTENFRSSTSTWGYSVGTSGALHEYADSOFGHIFAYGADRSEARKQ 500
DB 421 NPDTGFKPGMGALTENFRSSTSTWGYSVGTSGALHEYADSOFGHIFAYGADRSEARKQ 480

QY 501 MVISLKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSI 539
DB 481 MVISLKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSI
```

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RESULT 16
US-10-633-835-21
; Sequence 21, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Ustilago maydis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(519)
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 42-560)
US-10-633-835-21

Query Match          92.7%; Score 2694; DB 4; Length 519;
```

Best Local Similarity 100.0%; Pred. No. 5.6e-235;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 VLICNNGIAAIVEKIRKWAYETFGDERAIEFTVWATPEDLKVNADYIRMDQVYVEVPG 100
Db 1 VLICNNGIAAIVEKIRKWAYETFGDERAIEFTVWATPEDLKVNADYIRMDQVYVEVPG 60

QY 101 GSNNNYANVDLVDVAERAGVHVAWAGHASENPRLPESLAASKHKIIFIGPPGSAMR 160
Db 61 GSNNNYANVDLVDVAERAGVHVAWAGHASENPRLPESLAASKHKIIFIGPPGSAMR 120

QY 161 SLGDKISSTIVAHADVPQWPNSTGIGKTMMSDQGLTVSDVYQACIHTAEGLEKA 220
Db 121 SLGDKISSTIVAHADVPQWPNSTGIGKTMMSDQGLTVSDVYQACIHTAEGLEKA 180

QY 221 EKIGYPMVKASEGGGGKIRKCTNGEEFKQLYNVAGVPGSPVFMKLAGQARHLEVQ 280
Db 181 EKIGYPMVKASEGGGGKIRKCTNGEEFKQLYNVAGVPGSPVFMKLAGQARHLEVQ 240

QY 281 LLADQYGNASISIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEEAAVRLAKLVGYVSG 340
Db 241 LLADQYGNASISIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEEAAVRLAKLVGYVSG 300

QY 341 TWEWLYSPESGFAFLELNPRLQVHEPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLY 400
Db 301 TWEWLYSPESGFAFLELNPRLQVHEPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLY 360

QY 401 GMDPRGNEVIDPDSFSSPESFKTQKPOQGHVACRITAENPDGFKPGMGALTELNFRS 460
Db 361 GMDPRGNEVIDPDSFSSPESFKTQKPOQGHVACRITAENPDGFKPGMGALTELNFRS 420

QY 461 STSTWGYESVGTSGALHYADVSQGHIPAYGADRSEARKQWVISLKELSIRGDFRTTVEY 520
Db 421 STSTWGYESVGTSGALHYADVSQGHIPAYGADRSEARKQWVISLKELSIRGDFRTTVEY 480

QY 521 LIKLETDAPESNKITTCWLDGLIQDRLTAERPDLAV 559
Db 481 LIKLETDAPESNKITTCWLDGLIQDRLTAERPDLAV 519

RESULT 17
US-10-633-835-53
; Sequence 53, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(571)
; OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase BC domain (AAs 22-591)
US-10-633-835-53

Query Match 74.4%; Score 2163; DB 4; Length 571;
Best Local Similarity 73.5%; Pred. No. 9.3e-187;
Matches 408; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 5 HKAVSQFIGNPLETAPASPVADPFRKQGHVSITKVLICNNGIAAIVEKIRKWAYET 64
Db 1 HKAVSQFIGNPLETAPASPVADPFRKQGHVSITKVLICNNGIAAIVEKIRKWAYET 86

Db 17 HKIADHPFIGNPLENAPPSKVKEWVAHDGHTVITNVLNANGIAAIVEKIRSVRKWAYET 76
QY 65 FGDERAIEFTVWATPEDLKVNADYIRMDQVYVEVPGSGNNNNYANVDLVDVAERAGVHA 124
Db 77 FGDERAIEFTVWATPEDLKVNADYIRMDQVYVEVPGSGNNNNYANVDLVDVAERAGVHA 136

QY 125 VWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSIGDKISSTIVAHADVPQWPNSTG 184
Db 137 VWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSIGDKISSTIVAHADVPQWPNSTG 196

QY 185 TGIKETWMSDQGLTVSDVYQACIHTAEGLEKAEGKIGYPMVKASEGGGGKIRKCT 244
Db 197 TGVDAVQIDKGIIVTDDTTAKGCVTSWQGLEKARQIGFPVMIKASEGGGGKIRKAV 256

QY 245 NGEFKQLYNVAGVPGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSVORRHQ 304
Db 257 SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNASISIFGRDCSVORRHQ 316

QY 305 KIIIEAPVTIAPEDARESMEEAAVRLAKLVGYVSGAGTVEWLYSPESGFAFLELNPRLQV 364
Db 317 KIIIEAPVTIAPEDARESMEEAAVRLAKLVGYVSGAGTVEWLYSHADDDKFFYLELNPRLQV 376

QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDPDSFSSPESFKTOR 424
Db 377 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDPDSFSSPESFKTOR 436

QY 425 KPOQGHVACRITAENPDGFKPGMGALTELNFRSSTSTWGYESVGTSGALHYADVSQGH 484
Db 437 RPSKGLHTACRITSDPGEFGKPSNGVMHNLFRSSNVWGYFSGVGTQGGHHSFDSQF 496

QY 485 GHIPAYGADRSEARKQWVISLKELSIRGDFRTTVEYLIKLETDAPESNKITTCWLDGLI 544
Db 497 GHIPAYGADRSEARKQWVISLKELSIRGDFRTTVEYLIKLETDAPESNKITTCWLDGLI 556

QY 545 QDRLTAERPDLAV 559
Db 557 SKKLTAEPRDKMLAV 571

RESULT 18
US-10-633-835-52
; Sequence 52, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(581)
; OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592)
US-10-633-835-52

Query Match 74.4%; Score 2163; DB 4; Length 581;
Best Local Similarity 73.5%; Pred. No. 9.6e-187;
Matches 408; Conservative 59; Mismatches 88; Indels 0; Gaps 0;

QY 5 HKAVSQFIGNPLETAPASPVADPFRKQGHVSITKVLICNNGIAAIVEKIRSVRKWAYET 64
Db 27 HKIADHPFIGNPLENAPPSKVKEWVAHDGHTVITNVLNANGIAAIVEKIRSVRKWAYET 86

QY 65 FGDRAIAFTVWATPDLKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHA 124
 DB 87 FGDRAIOFTVWATPDLKANADYIRMDHYVEVPGGNNNNYANVELIVDAERNVHA 146
 QY 125 VWAGHGHAENPRLPESLAASKHIIIFGPPGSAMRSLGDKISSTIIVAHADVPCMPWSG 184
 DB 147 VWAGHGHAENPRLPESLAASKHIIIFGPPGSAMRSLGDKISSTIIVAHADVPCMPWSG 206
 QY 185 TGIKETMMSDQGLTVSDVYQOACIHTABEGLEKAEKIGYPMVKASEGGGKIRKCT 244
 DB 207 TGVDAVQIDKKGIVTVDDTYAKGCVTSWQEGLEKARQIGFPVMIKASEGGGKIRKAV 266
 QY 245 NGEFPOKLYNAVLGEVPGSPVFMKLAGOARHLEVOLLADQYGNNAISIFGRDCSVORRHQ 304
 DB 267 SEEGFEELYKAAASEIPGSPFIMKLAGNARHLEVOLLADQYGNNAISIFGRDCSVORRHQ 326
 QY 305 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGVVSAGTVEWLYSPESGGEFAFLELNPRLQV 364
 DB 327 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGVVSAGTVEWLYSPESGGEFAFLELNPRLQV 386
 QY 365 EHPTEGVSVGNVPAQQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTOR 424
 DB 387 EHPTEGVSVGNVPAQQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTOR 446
 QY 425 KPOQGHVACHITAEINPDGTGKPGMGALTELNFRSSSTSTWGYFSGTSGALHEVADSQF 484
 DB 447 RPSKGLHTACRITSEDGEGFKPSNGVMHLELNFSSSNVWGVSVGTQGGIHSFSDSQF 506
 QY 485 GHIPAYGADRSEARKOMVISIKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTCGLDGLI 544
 DB 507 GHIPAYGADRSEARKOMVISIKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTCGLDGLI 566
 QY 545 QDRLTAERPPADLAV 559
 DB 567 SKLTAERPPDKMLAV 581
 RESULT 19
 US-10-633-835-6
 ; Sequence 6, Application US/10633835
 ; Publication No. US20040086994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elich, Tedd D.
 ; APPLICANT: Volrath, Sandra L.
 ; APPLICANT: Weatherly, Stephanie C.
 ; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
 ; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
 ; FILE REFERENCE: 9280.2
 ; CURRENT APPLICATION NUMBER: US/10/633,835
 ; CURRENT FILING DATE: 2003-08-04
 ; PRIOR APPLICATION NUMBER: US 60/401,170
 ; PRIOR FILING DATE: 2003-08-05
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Magnaporthe oryzae
 US-10-633-835-6

Query Match 74.4%; Score 2163; DB 4; Length 591;
 Best Local Similarity 73.5%; Pred. No. 9.9e-187;
 Matches 408; Conservative 59; Mismatches 88; Indels 0; Gaps 0;

QY 5 HKAVSQFIGNPLETAPASPVADPIRKQGGHSVITKVICNNGIAAVERISIRKWAYET 64
 DB 37 HKIADHFTGGARLENAPPSKVKEWVAHDGHTVITNVLIANNIAAVERISIRKWAYET 96
 QY 65 FGDRAIAFTVWATPDLKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHA 124
 DB 97 FGDRAIOFTVWATPDLKANADYIRMDHYVEVPGGNNNNYANVELIVDAERNVHA 156

QY 125 VWAGHGHAENPRLPESLAASKHIIIFGPPGSAMRSLGDKISSTIIVAHADVPCMPWSG 184
 DB 157 VWAGHGHAENPRLPESLAASKHIIIFGPPGSAMRSLGDKISSTIIVAHADVPCMPWSG 216
 QY 185 TGIKETMMSDQGLTVSDVYQOACIHTABEGLEKAEKIGYPMVKASEGGGKIRKCT 244
 DB 217 TGVDAVQIDKKGIVTVDDTYAKGCVTSWQEGLEKARQIGFPVMIKASEGGGKIRKAV 276
 QY 245 NGEFPOKLYNAVLGEVPGSPVFMKLAGOARHLEVOLLADQYGNNAISIFGRDCSVORRHQ 304
 DB 277 SEEGFEELYKAAASEIPGSPFIMKLAGNARHLEVOLLADQYGNNAISIFGRDCSVORRHQ 336
 QY 305 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGVVSAGTVEWLYSPESGGEFAFLELNPRLQV 364
 DB 337 KIIEAPVTIAPEDARESEMEKAAVRLAKLVGVVSAGTVEWLYSPESGGEFAFLELNPRLQV 396
 QY 365 EHPTEGVSVGNVPAQQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTOR 424
 DB 397 EHPTEGVSVGNVPAQQLQVAMGIPLYSIRDITLYGMDPRGNEVIDDFSSPESFQTOR 456
 QY 425 KPOQGHVACHITAEINPDGTGKPGMGALTELNFRSSSTSTWGYFSGTSGALHEVADSQF 484
 DB 457 RPSKGLHTACRITSEDGEGFKPSNGVMHLELNFSSSNVWGVSVGTQGGIHSFSDSQF 516
 QY 485 GHIPAYGADRSEARKOMVISIKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTCGLDGLI 544
 DB 517 GHIPAYGADRSEARKOMVISIKELSIKELSGIRGDFRTTVEYLIKLETDAPESNKITTCGLDGLI 576
 QY 545 QDRLTAERPPADLAV 559
 DB 577 SKLTAERPPDKMLAV 591
 RESULT 20
 US-10-369-493-3698
 ; Sequence 3698, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 3698
 ; LENGTH: 2301
 ; TYPE: PRT
 ; ORGANISM: Neurospora crassa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(2301)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-10-369-493-3698

Query Match 73.6%; Score 2139; DB 4; Length 2301;
 Best Local Similarity .688%; Pred. No. 1.2e-183;
 Matches 411; Conservative 58; Mismatches 86; Indels 42; Gaps 2;

QY 5 HKAVSQFIGNPLETAPASPVADPIRKQGGHSVIT-----KVLII 43
 DB 6 HNLAPHFIGNRLENAPPSKVKEWVAHDGHTVITNVRLAPAVQVTRFXHLVFLVQLI 65
 QY 44 CNNGIAAVERISIRKWAYETFGDERAIEFTVMATPDLKVNADYIRMDQYVEVPGGNN 103
 DB 66 ANGLIAAVERISIRKWAYETFGDERAIEFTVMATPDLKVNADYIRMDQYVEVPGGNN 125

Qy	104	NNNYANVDLIVDAERAGVHAWAGH-----GHASENPRLPESL	141
Db	126	NNHYANVELIVDAERMDVHAWAGCVDKSPASGVDMGKILTVIRGCHASENPKLPESL	185
Qy	143	AASKHKIIPGPPGSAMRSLGDKISSTIVAQADVPCMPWSGTGIGKETWMSDQGLTVSD	202
Db	186	AASPKKIVFIPGGSAMRSLGDKISSTIVAQADVPCI PWSGTGIVSEVVDONGIVTVPD	245
Qy	203	DVYQOACIHTABEGLEKAKKIGVPMVIKASGEGGGKIRKCTNGBEFKOLYNAVILGEVPG	262
Db	246	DVYLGCVSSWOEGLEKAREIGFPPVMIKASGEGGGKIRKVLNEDNFESLYNAAASEIPG	305
Qy	263	SPVFWKLAGARHLEVQLLADQYGNASISIFGRDCSVORRHOKIIEEAPVTTAPEDARES	322
Db	306	SPIFIMKLADSARHLEVQLLADQYGNNSLFGDCSVORRHOKIIEEAPVTTAKPMTFKA	365
Qy	323	MEKAAVRLAKLVGYVSAGTVEVLYSPESGEFAFLELNPRLQVEHPTEMTMSGVNIIPAQOL	382
Db	366	MEEAAVRLGRLVGYVSAGTVEVLYSHADDKFYFLELNPRLQVEHPTEMTMSGVNLPAQOL	425
Qy	383	QVAMGIPLYSIRDITRLCYMDPRGNEVIDDFDSSPESFKTQRKPOQGHVACRITAENP	442
Db	426	QVAMGIPLHRINDIRLLYGVDPRTASEIDFEPKNPESEKTOBRPTPKGHTTACRITSEDP	485
Qy	443	DTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYCADRSEARKOWY	502
Db	486	GEGFKPSNGVLHDLNFRSSSNVWGYFSVGSAGGIHSPDSQFGHIFAYGENRAAERKHVY	545
Qy	503	ISLKELSIRGRDPRITVEVYLKLETDAPESNKITTWGLDGLIOBRLTAERPPADIAV	559
Db	546	VALKELSIRGRDPRITVEVYLKLETAPEENTITTWGLDELSIKKLTARPDPIIAV	602

```

RESULT 21
US-10-633-835-54
; Sequence 54, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(581)
; OTHER INFORMATION: C-terminal deleted Magnaporthe ACCase (AAS 2-582)
US-10-633-835-54

```

	Query Match	73.4%	Score 2135;	DB 4;	Length 581;
	Best Local Similarity	73.6%;	Pred. No. 3.3e-184;		
	Matches 401;	Conservative	59;	Mismatches 85;	Indels 0; Gaps 0;
Qy	5	HKAVSQPIGNNPLETAPASPVADPIRQGGHSVITKVLICNNGIAAANKETRSIRKWAYET	64		
Db	37	HK1ADHF1GGNNLENAPPSKVKEWAHDGHTVTNVLIANNGIAAANKETRSVSRKWAYET	96		
Qy	65	FGDERAL1EFTVMTATPEDLKVNADYIRMAADQVVEVPGGSNNNNYANVDLI1VDVAERAGVHA	124		
Db	97	FGDERALQFTVMTATPEDLQANADYIRMAADHYVEVPGGTNNNNYANVELLI1VDVAERMNVHA	156		
Qy	125	VWAGWGCHASENPL1PESLAASKHKH11FI1GPPGGSAMRSLIGDKISST11VAQIADVCPMPWSG	184		

[illegible]

```

RESULT 22
US-10-633-835-55
; Sequence 55, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(571)
; OTHER INFORMATION: C-terminal deleted Magnaporthe ACCase BC domain (AAS 2-572)
US-10-633-835-55

```

Query Match	72.5%	Score 2109;	DB 4;	Length 571;
Best Local Similarity	73.8%;	Pred. No. 7.4e-182;		
Matches 395;	Conservative 58;	Mismatches 82;	Indels 0;	Gaps 0;
QY	5	HKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKGISSIRKWAYET	64	
Db	37	HKIDHFIGGNLENAPPSSKVKEWAHDGHTVIITNVLNANGIAAVKGISSIRKWAYET	96	
QY	65	FGDERAIEFTVMATPEDLKNADYIRMDAQYVEVPGSGNNNNYANYDLIDVVAERAGVHA	124	
Db	97	FGDERAIQFTVMATPEDLQANADYIRMDAHYVEVPGGTNNNNYANVELIYDVAERNVHA	156	
QY	125	VWAGHGHAASENPRLPESLAASKHKHIIFTGPPGSAMRSLGDKSIISTTVAQHADVPCMPWSG	184	

Query Match	70.9%;	Score 2060;	DB 4;	Length 560;
Best Local Similarity	69.1%;	Pred. No. 2e-177;		
Matches 386;	Conservative 76;	Mismatches 89;	Indels 8;	Gaps 3;
QY	3	PDHKAVSQFTGGNPLETAPASPVAADFTRKOGGSHSVITKVLICNNGIAAIVKEIRSRWAY	62	
Db	8	PGH-----FGLNTVDKLESLPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSVRWAY	62	
QY	63	ETFGDERAIEFTVMATPEDLKVNADYIRMDAQYVEVPGGSNNNNYANVDLIVDVAERAGV	122	
Db	63	ETFGDRTVQVAMATPEDLLEANAERYIRMDAQYIEVPGGTNNNNYANVDLIVDIAERADV	122	
QY	123	HAYWAGGHASENPLRPESLAASKHKILFTGPGCSAMRSIGDKISSTIVIAQHADVPCMPW	182	
Db	123	DAWAGGHASENPLRPEKLSQSKRKVIFITGPGGNAMRSIGDKISSTIVIAQSAKVPICPW	182	
QY	183	SGTGIKETWMSDQ--GFLTIVSDVYQACLIHTAEGLKEAKGICYPVMIKASEGGGKGKI	240	
Db	183	SGTGV--DTVHDEKTVGLSVDDDIYQGCCTSDPEDGLQKAKRIGFPPVMIKASEGGGKGKI	241	
QY	241	RKCTNGEFPQLYNVVLGEVPGSPVFMVLAGQARHLEVLLADQYGNALISIFGRDCSVQ	300	
Db	242	QVVERBEDFALYHQAAANEIPGSPFITMKLAGRARHLEVLLADQYGTNISLFRDCSVQ	301	
QY	301	RRHQKIIIEAPVTIAPEDARESMEKAIVRLAKLVGYYSAGTVEWMLYSPGESGFAFLINP	360	
Db	302	RRHQKIIIEAPVTIAKAEETHEMEKAIVRLKLVGYYSAGTVEYLYSHDDKCFYFLINP	361	

Query Match	70.9%;	Score 2060;	DB 4;	Length 570;
Best Local Similarity	69.1%;	Pred. No. 2e-177;		
Matches	386;	Conservative	76;	Mismatches 89;
			Indels	8;
			Gaps	3;

QY	3	POHKAVSQFIGGNPLETAPASPVADPIRKOGGHSVITKVLICNNGIAAIVKEIRSIRKWAY	62
DB	18	PGH-----FIGLTVDKLBEESPURDFVKSGGHTVISKILIANNGIAAIVKEIRSVRKWAY	72
QY	63	ETFGDERAJEFTWMAETPEDLKVNADEVIRMAQVVEVPGGSNNNNYANVDLLIVDVAERAGV	122
DB	73	ETFGDDRTVQFVAMATPEDLEANADEVIRMAQVIEVPGGTNNNNYANVDLLIVDAERADV	132
QY	123	HAVWAGWGHASENPRUPESLAASKHKIIFTPGPGSAMRSIGDKISSTIVAQHADVPCCMPW	182
DB	133	DAVWAGWGHASENPLLPKELQSQRKVIFFTPGPGNAMRSIGDKISSTIVAQSAKVPCTPW	192
QY	183	STGTGKETWMSDQ--GFLTVSDDDVYQACIHTAEGLKAEKIGYPWMIKASEGGGGKGI	240
DB	193	STGTG-DTVHVDKTLGVSDDDIYQGGCTSPEDGLQAKRIGFPWMIKASEGGGGKGI	251
QY	241	RKCTNGEEFKQLYNAVILGVPGSVPVWMLAGQARHLEVOLLADQYGNALISIFGRDCSVQ	300
DB	252	RQVEREEDFIALYHQAAEIPGSPFIIMKLACHARHLEVOLLADQYGTNLSLGRDCSVQ	311
QY	301	RRHQKIIIEAPVTIAPEDARESMKEAAVRLAKLVGVYSAGTVLWYSPSGEFAFLBNP	360
DB	312	RHOKIIEBAPVTIAKAEFTFHEMKAARGLKLVGVYSAGTVLYSHDDGKFFYLENP	371

QY 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
DB 372 RLOVEHPTTEMVSGVNLPAALQIANGIPMHRISDIRTYLGMNPHSASEIDFEFKTQDAT 431
QY 421 KTORPOQOHHVACRIITAEENPDTPGPKGMCALTELNFSSNSTWGYFSGALHEYA 480
DB 432 KQORRPIPKGHCTACRITSEDPNDGPKPGGTLHELNFSSNVWGYFSGVNGNIHFS 491
QY 481 DSQFGHIFAYGADRSEARKQWISLKELSGIRGDFRTTVEYLLKLETTDAFESNKITTCWL 540
DB 492 DSQFGHIFAFGENROASRKHMVVALKELSGIRGDFRTTVEYLLKLETTEDFEDNTTTCWL 551
QY 541 DGLIQDLTLAERPPADLAV 559
DB 552 DDLITHQMTAEKPDPTLAV 570

RESULT 27

US-10-633-835-33
; Sequence 33, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(575)
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAE
; OTHER INFORMATION: 7-581)
US-10-633-835-33

Query Match 70.9%; Score 2060; DB 4; Length 575;
Best Local Similarity 69.1%; Pred. No. 2.1e-177; Mismatches 89; Indels 8; Gaps 3;
Matches 396; Conservative 76; Mismatches 89; Indels 8; Gaps 3;
QY 3 PDHKAVSQFIGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAA VKEIRSKWAY 62
DB 23 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSKWAY 77
QY 63 ETFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERAGV 122
DB 78 ETFGDDRTVQFVAMATPEDEANAEYIRMDQYIEVPGGNNNNYANVDLI DVIAERADV 137
QY 123 HAVWAGHGHASENPRLPESLAASKHIIIFIGPPGSAMRSLGDKISSTIVAOHADVP CPMW 182
DB 138 DAVWAGHGHASENPRLPEKLSQSKRVIFIGPPGNMRSGLGDKISSTIVAO SAKVPCIPW 197
QY 183 SGTGKETMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGKI 240
DB 198 SGTGV-DTVHVDKTLGVSDVDDIYQGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGKI 256
QY 241 RKTNGEPEFKQLYNALGEVPGSPFVWMLAGARHLEVQLLADQYGNALISIFGRDCSVQ 300
DB 257 RQVEREEDFIALYHQAANEIPGSPFIMKLAGRARHLEVQLLADQYGTNISLFGDCSVQ 316
QY 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVSAGTVWLYSPESGEFAFLELNP 360
DB 317 RRHOKIIEEAPVTIAKAEFTHEMEKAAVRLKLVGVSAGTVWLYSHDDGKFYFLELNP 376

RESULT 28

US-10-633-835-8
; Sequence 8, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-633-835-8

Query Match 70.9%; Score 2060; DB 4; Length 580;
Best Local Similarity 69.1%; Pred. No. 2.1e-177; Mismatches 89; Indels 8; Gaps 3;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

QY 3 PDHKAVSQFIGNPLETAPASPVADFIKQGGHSHVITKVLICNNGIAA VKEIRSKWAY 62
DB 28 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAA VKEIRSKWAY 82
QY 63 ETFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGGNNNNYANVDLI DVVAERAGV 122
DB 83 ETFGDDRTVQFVAMATPEDEANAEYIRMDQYIEVPGGNNNNYANVDLI DVIAERADV 142
QY 123 HAVWAGHGHASENPRLPESLAASKHIIIFIGPPGSAMRSLGDKISSTIVAOHADVP CPMW 182
DB 143 DAVWAGHGHASENPRLPEKLSQSKRVIFIGPPGNMRSGLGDKISSTIVAO SAKVPCIPW 202
QY 183 SGTGKETMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGKI 240
DB 203 SGTGV-DTVHVDKTLGVSDVDDIYQGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGKI 261
QY 241 RKTNGEPEFKQLYNALGEVPGSPFVWMLAGARHLEVQLLADQYGNALISIFGRDCSVQ 300
DB 262 RQVEREEDFIALYHQAANEIPGSPFIMKLAGRARHLEVQLLADQYGTNISLFGDCSVQ 321
QY 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVSAGTVWLYSPESGEFAFLELNP 360
DB 322 RRHOKIIEEAPVTIAKAEFTHEMEKAAVRLKLVGVSAGTVWLYSHDDGKFYFLELNP 381
QY 361 RLOVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDFSSPSF 420
DB 382 RLOVEHPTTEMVSGVNLPAALQIANGIPMHRISDIRTYLGMNPHSASEIDFEFKTQDAT 441

QY 421 KTORQPQGHVACRITAEINPDGFKPGMGALTELNFRSSTSTWGYFSGVTSGALHEYA 480
DB 442 KKORRPIPKGHCTACRITSEDNDGFKPSGGTLHELNFRSSNVWGYFSGVNGNHNHFS 501
QY 481 DSOFGHIIFAYGADRSEARKOMVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTCWL 540
DB 502 DSOFGHIIFAYGADRSEARKOMVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTCWL 561
QY 541 DGLIQLRLTAERPPADLAV 559
DB 562 DDLITHKMTAEKDPDTLAV 580

RESULT 29
US-10-369-493-1998
; Sequence 1998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 2002-02-21
; SEQ ID NO 1998
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1998

Query Match 70.9%; Score 2060; DB 4; Length 2233;
Best Local Similarity 69.1%; Pred. No. 1.7e-176;
Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;

QY 3 PDHKAVSQFIGNPLETAPSPVADFKKOGHSHVITKVLICNNGIAAVERKIRKWAY 62
DB 29 PGH-----FIGLNTVDKLEESPLDFVKSHGHVTSKILLIANNNGIAAVERKIRKWAY 83

QY 63 ETFGDERAIEFTVATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGV 122
DB 84 ETFGDDRTVQFVATPEDLEANAERYIRMDQYIEVPGGNNNNYANVDLIVDAERADV 143

QY 123 HAVWAGHASENPRLPESLAASKHIIIFGPPGSAKRSKISSTIVAGHADVPKMPW 182
DB 144 DAVWAGHASENPLLPESLAASKHIIIFGPPGSAKRSKISSTIVAGHADVPKMPW 203

QY 183 SGTGIRKTEMSDQ--GFLTVSDVYVQACIHTAEGLKAEKIGYVPMIKASEGGGKGI 240
DB 204 SGTGV-DTVHDEKTVGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 262

QY 241 RKTNGEEFQQLNAVIGVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 300
DB 263 ROVEREEDFTALYHQAAANEIPGSPFIFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 322

QY 301 RHOKLIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNP 360
DB 323 RHOKLIEEAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVWLYSHDDGKPFYFLELNP 382

QY 361 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVDIDFSSPESF 420
DB 383 RLQVEHPTTMSGVNIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVDIDFSSPESF 442

QY 421 KTORQPQGHVACRITAEINPDGFKPGMGALTELNFRSSTSTWGYFSGVTSGALHEYA 480
DB 443 KKORRPIPKGHCTACRITSEDNDGFKPSGGTLHELNFRSSNVWGYFSGVNGNHNHFS 502

QY 481 DSOFGHIIFAYGADRSEARKOMVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTCWL 540
DB 503 DSOFGHIIFAYGADRSEARKOMVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTCWL 562

QY 541 DGLIQLRLTAERPPADLAV 559
DB 563 DDLITHKMTAEKDPDTLAV 581

RESULT 30
US-10-633-835-36
; Sequence 36, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 36
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(550)
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A
; OTHER INFORMATION: 32-581
US-10-633-835-36

Query Match 70.8%; Score 2058.5; DB 4; Length 550;
Best Local Similarity 69.7%; Pred. No. 2.6e-177;
Matches 384; Conservative 76; Mismatches 88; Indels 3; Gaps 2;

QY 11 FIGNPLETAPSPVADFKKOGHSHVITKVLICNNGIAAVERKIRKWAYETFGDERA 70
DB 1 FIGLNTVDKLEESPLDFVKSHGHVTSKILLIANNNGIAAVERKIRKWAYETFGDDRT 60

QY 71 IFTVMTATPEDLKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHAWAGW 130
DB 61 VQFVMTATPEDLEANAERYIRMDQYIEVPGGNNNNYANVDLIVDAERADVDVWAGW 120

QY 131 HASENPLLPESLAASKHIIIFGPPGSAKRSKISSTIVAGHADVPKMPWGTGKET 190
DB 121 HASENPLLPESLAASKHIIIFGPPGSAKRSKISSTIVAGHADVPKMPWGTGKV-DT 179

QY 191 MMSDQ--GFLTVSDVYVQACIHTAEGLKAEKIGYVPMIKASEGGGKIRKCTNGEE 248
DB 180 VHVDEKTVGLSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKIRKCTNGEE 239

QY 249 FKQLNAVIGVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQRHOKIIE 308
DB 240 FKQLNAVIGVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQRHOKIIE 299

QY 309 EAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNPLOVEHPT 368
DB 300 EAPVTIAPEDARESEKAAVRLAKLVGYVSAGTVWLYSHDDGKPFYFLELNPLOVEHPT 359

QY 369 TEMVSGVNIIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVDIDFSSPESFQTKRKP 428
DB 360 TEMVSGVNIIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVDIDFSSPESFQTKRKP 419

QY 429 OGHVACRITAEINPDGFKPGMGALTELNFRSSTSTWGYFSGVTSGALHEYADSQGHIF 488
DB 420 KGHCTACRITSEDNDGFKPSGGTLHELNFRSSNVWGYFSGVNGNHNHFS 479

QY 489 AYGADESEARKOMVLSKELSRGDFRTTVEYLKLETDAPESNKITTCWLDGLIQDRL 548
DB 480 APGENQASRKHMVVALKELSRGDFRTTVEYLKLETDAPESNKITTCWLDGLITHKM 539
QY 549 TAERPPADLAV 559
DB 540 TAERPDPTLAV 550

RESULT 31
US-10-633-835-32
; Sequence 32, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (76)..(76)
; OTHER INFORMATION: Saccharomyces cerevisiae ACCase BC domain S77Y mutation
US-10-633-835-32

Query Match 70.7%; Score 2054; DB 4; Length 580;
Best Local Similarity 68.9%; Pred. No. 7, 4e-177; Indels 8; Gaps 3;
Matches 385; Conservative 76; Mismatches 90;

QY 3 PDHKAVSOFIGNPLETAPSPVADFIKOGHSHVITKVLICNNNGIAAIVKESIRKWAY 62
DB 28 PGH-----FIGLTVDKLEESPLRDFVKSHGGHTVISKILLIANNGIAAIVKESIRKWAY 82

QY 63 ETFGDERAIEFTVMATPEDLKVNADYIRMAQYVEVPGSSNNNNYANVDLIVDAERAGV 122
DB 83 ETFGDDRTVQVFMATPEDLEANAERYIRMAQYIEVPGGTNNNNYANVDLIVDAERADV 142

QY 123 HAVWAGWGHASENPLPESLAASKHIIIFGPPGSAEMLGDKISSTIVAGHADVPICPW 182
DB 143 DAVWAGWGHASENPLPESLQSKKRVIFGPPGNAMSLGDKISSTIVAGSAKVPCIPW 202

QY 183 SGTGKETMMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPMVIMKASEGGGKGI 240
DB 203 SGTGV-DTVHVDKTVGLSVDDDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGI 261

QY 241 RKTNGEEFKQLYNAVLEVPGPSVFMKLAGQARHLEVQLLADQYGNALIFGRDCSVQ 300
DB 262 ROVEREEDFIALYHQAAANEIPGSPFIIMKLAGARHLEVQLLADQYGTNIFLGRDCSVQ 321

QY 301 RRHQKIIIEAPVTIAPEDARESMERKAARLAKLVGYVSAGTVEMLYSPESGEFAFLELNP 360
DB 322 RRHQKIIIEAPVTIAPEDARESMERKAARLAKLVGYVSAGTVEMLYSHDDGKFYLELNP 381

QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDFDSSPSF 420
DB 382 RLQVEHPTTEMVSGVNLPAALQIANGIPMHRISDIRTYGMNPHSAEIDFEFTQDAT 441

QY 421 KTQKPOQGHVACRIATENPDGFKPGMGALTEINFRSSTSTWGVSVGTSGALHEYA 480
DB 442 KQRRPIPKGHCTACRITSEDNDGFKPSGGTLHELNFRSSNVWGYFVSGNNGNIHFS 501

QY 481 DSQFGHIFAYGADRSEARKQMVLSKELSRGDFRTTVEYLKLETDAPESNKITTCWLD 540

DB 502 DSQFGHIFAYGADRSEARKQMVLSKELSRGDFRTTVEYLKLETDAPESNKITTCWLD 561
QY 541 DGLIQLDLTAERPPADLAV 559
DB 562 DDLITHQWTAERKPDPTLAV 580

RESULT 32
US-10-633-835-44
; Sequence 44, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(570)
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
; OTHER INFORMATION: domain (AAs 7-576)
US-10-633-835-44

Query Match 70.6%; Score 2051; DB 4; Length 570;
Best Local Similarity 69.3%; Pred. No. 1, 3e-176; Indels 8; Gaps 3;
Matches 383; Conservative 76; Mismatches 86;

QY 3 PDHKAVSOFIGNPLETAPSPVADFIKOGHSHVITKVLICNNNGIAAIVKESIRKWAY 62
DB 23 PGH-----FIGLTVDKLEESPLRDFVKSHGGHTVISKILLIANNGIAAIVKESIRKWAY 77

QY 63 ETFGDERAIEFTVMATPEDLKVNADYIRMAQYVEVPGSSNNNNYANVDLIVDAERAGV 122
DB 78 ETFGDDRTVQVFMATPEDLEANAERYIRMAQYIEVPGGTNNNNYANVDLIVDAERADV 137

QY 123 HAVWAGWGHASENPLPESLAASKHIIIFGPPGSAEMLGDKISSTIVAGHADVPICPW 182
DB 138 DAVWAGWGHASENPLPESLQSKKRVIFGPPGNAMSLGDKISSTIVAGSAKVPCIPW 197

QY 183 SGTGKETMMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPMVIMKASEGGGKGI 240
DB 198 SGTGV-DTVHVDKTVGLSVDDDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGKGI 256

QY 241 RKTNGEEFKQLYNAVLEVPGPSVFMKLAGQARHLEVQLLADQYGNALIFGRDCSVQ 300
DB 257 ROVEREEDFIALYHQAAANEIPGSPFIIMKLAGARHLEVQLLADQYGTNIFLGRDCSVQ 316

QY 301 RRHQKIIIEAPVTIAPEDARESMERKAARLAKLVGYVSAGTVEMLYSPESGEFAFLELNP 360
DB 317 RRHQKIIIEAPVTIAPEDARESMERKAARLAKLVGYVSAGTVEMLYSHDDGKFYLELNP 376

QY 361 RLQVEHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDFDSSPSF 420
DB 377 RLQVEHPTTEMVSGVNLPAALQIANGIPMHRISDIRTYGMNPHSAEIDFEFTQDAT 436

QY 421 KTQKPOQGHVACRIATENPDGFKPGMGALTEINFRSSTSTWGVSVGTSGALHEYA 480
DB 437 KQRRPIPKGHCTACRITSEDNDGFKPSGGTLHELNFRSSNVWGYFVSGNNGNIHFS 496

QY 481 DSQFGHIFAYGADRSEARKQMVLSKELSRGDFRTTVEYLKLETDAPESNKITTCWLD 540

Db 497 DSQGHIFAFGENRQASRKHVMVVALKELSIKRGDFRTTVEYLKLETFEDFEDNTITGWL 556
Qy 541 DGLIQDRLTAERP 553
Db 557 DDLITHKMTAERP 569

RESULT 33
US-10-633-835-38
; Sequence 38, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(575)
; OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
; OTHER INFORMATION: 2-576)
US-10-633-835-38

Query Match 70.6%; Score 2051; DB 4; Length 575;
Best Local Similarity 69.3%; Pred. No. 1.4e-176;
Matches 383; Conservative 76; Mismatches 86; Indels 8; Gaps 3;
Qy 3 PDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAVKEIRSIRKWAY 62
Db 28 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY 82
Qy 63 ETFGDERAIEFTVMATPEDLVKNADYIRMAQYIEVPGSGNNNNYANVDLIVDAERAGV 122
Db 83 ETFGDDRTVQVAMATPEDLEANAERYIRMAQYIEVPGGTNNNNYANVDLIVDAERADV 142
Qy 123 HAVWAGHGHASENPLPESLAASKHKIIFIGPGSAMRSLGDKISSTIVAOHADVPICMPW 182
Db 143 DAVWAGHGHASENPLPESLAASKHKIIFIGPGSAMRSLGDKISSTIVAOHADVPICMPW 202
Qy 183 SGTGKETMMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPMVMIKASEGGGKGI 240
Db 203 SGTGV-DTVHVDKTLGVSDVDDIYQKCCTSPEGLQAKRIGFPPVMIKASEGGGKGI 261
Qy 241 RKTNGEEFKOLYNAVIGEVPGSPVFMVLMKLAGARHLEVQLLADQYGNALISIFGRDCSVQ 300
Db 262 RQVEREDFTALYHQAAANEIPGSPFIFIMKLARHLEVQLLADQYGNALISIFGRDCSVQ 321
Qy 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEPAFLEINP 360
Db 322 RRHOKIIEEAPVTIATAETTHEMEKAAVRLKLVGVYSAGTVWLYSHDDGKGFYLEINP 381
Qy 361 RLQVEHPTTEMVSGVNIPLAAQLOVAMGIPLYSIDRTLYGMDPRGNEVIDDFDSSPESF 420
Db 382 RLQVEHPTTEMVSGVNIPLAAQLOVAMGIPWIRISDITLYGMNPHSASEIDFEKTDQAT 441
Qy 421 KTORKPOQGHVACRITAENPDTPGKPMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480
Db 442 KKQRRIIPKGHCTACRITSEDPNDGPKSGGTLHELNFRRSSNVWGYFSVGNNGNIHSPS 501
Qy 481 DSQFCHIFAYGADRSEARKQMWISLKELSIKRGDFRTTVEYLKLETFEDFESNKITGWL 540

Db 502 DSQGHIFAFGENRQASRKHVMVVALKELSIKRGDFRTTVEYLKLETFEDFEDNTITGWL 561
Qy 541 DGLIQDRLTAERP 553
Db 562 DDLITHKMTAERP 574

RESULT 34
US-10-633-835-43
; Sequence 43, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(575)
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
; OTHER INFORMATION: domain (AAs 4-578)
US-10-633-835-43

Query Match 70.6%; Score 2051; DB 4; Length 575;
Best Local Similarity 69.3%; Pred. No. 1.4e-176;
Matches 383; Conservative 76; Mismatches 86; Indels 8; Gaps 3;
Qy 3 PDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAVKEIRSIRKWAY 62
Db 26 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSIRKWAY 80
Qy 63 ETFGDERAIEFTVMATPEDLVKNADYIRMAQYIEVPGSGNNNNYANVDLIVDAERAGV 122
Db 81 ETFGDDRTVQVAMATPEDLEANAERYIRMAQYIEVPGGTNNNNYANVDLIVDAERADV 140
Qy 123 HAVWAGHGHASENPLPESLAASKHKIIFIGPGSAMRSLGDKISSTIVAOHADVPICMPW 182
Db 141 DAVWAGHGHASENPLPESLAASKHKIIFIGPGSAMRSLGDKISSTIVAOHADVPICMPW 200
Qy 183 SGTGKETMMSDQ--GFLTVSDVYQACIHTAEGLKAEKIGYPMVMIKASEGGGKGI 240
Db 201 SGTGV-DTVHVDKTLGVSDVDDIYQKCCTSPEGLQAKRIGFPPVMIKASEGGGKGI 259
Qy 241 RKTNGEEFKOLYNAVIGEVPGSPVFMVLMKLAGARHLEVQLLADQYGNALISIFGRDCSVQ 300
Db 260 RQVEREDFTALYHQAAANEIPGSPFIFIMKLARHLEVQLLADQYGNALISIFGRDCSVQ 319
Qy 301 RRHOKIIEEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEPAFLEINP 360
Db 320 RRHOKIIEEAPVTIATAETTHEMEKAAVRLKLVGVYSAGTVWLYSHDDGKGFYLEINP 379
Qy 361 RLQVEHPTTEMVSGVNIPLAAQLOVAMGIPLYSIDRTLYGMDPRGNEVIDDFDSSPESF 420
Db 380 RLQVEHPTTEMVSGVNIPLAAQLOVAMGIPWIRISDITLYGMNPHSASEIDFEKTDQAT 439
Qy 421 KTORKPOQGHVACRITAENPDTPGKPMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480
Db 440 KKQRRIIPKGHCTACRITSEDPNDGPKSGGTLHELNFRRSSNVWGYFSVGNNGNIHSPS 499
Qy 481 DSQFCHIFAYGADRSEARKQMWISLKELSIKRGDFRTTVEYLKLETFEDFESNKITGWL 540

Db 500 DSQGHIFAFGENQASRKMVVALKELSGRDFRTTVEYLKLETFEDNTITGWL 559
Qy 541 DGLIQDLRLTAERP 553
Db 560 DDLITHKWTAKP 572

RESULT 35

US-10-633-835-65
; Sequence 65, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 511
; TYPE: PRP
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(511)
; OTHER INFORMATION: N- and C-terminal deleted Magnaporthe ACCase BC domain (AAS
; OTHER INFORMATION: 72-582)
US-10-633-835-65

Query Match 70.4%; Score 2046; DB 4; Length 511;
Best Local Similarity 75.1%; Pred. No. 3.2e-176; Mismatches 55; Indels 0; Gaps 0;
Matches 384; Conservative 55; Mismatches 72; Indels 0; Gaps 0;
Qy 39 TKVLICNNGIAAVERKIRKWAYETFGDERAIEFTVMATPDLKVNADYIRMDQYVEV 98
Db 1 TNLVIANNGIAAVERKIRKWAYETFGDERAIEFTVMATPDLKANADYIRMDHYEV 60
Qy 99 POGSNNNNYANVDLIVDAERAGVAVWAGWGHASENRLPSLAASKHKIIFIGPPGSA 158
Db 61 PGSTNNNNYANVELIVDAERNVAVWAGWGHASENPKLPESLAASPKKIIFIGPPGSA 120
Qy 159 MRLSGDKISSTIVAGHADVPKMPWSTGTIKETMMSDQGLTVSDVYQACIHTAEGL 218
Db 121 MRLSGDKISSTIVAGHADVPKMPWSTGTVDVQIDKKGIVTVDDDTYAKGCVTSWQEGLE 180
Qy 219 KAEKIGYPMIKASGGGGKIRKCTNGEEFKQLYNALVGEVPGSPFVFMKLAGOARHLE 278
Db 181 KARQIGFPMIKASGGGGKIRKAVSEGFEEYKAAASEIPGSPFIMKLAGNARHLE 240
Qy 279 VOLLADQYGNALISIFGRDCSVORRHQKIIIEAPVTIAPEDARESMEKAARLAKLVGVYS 338
Db 241 VOLLADQYGNISLFGDCSVORRHQKIIIEAPVTIAPEDARESMEKAARLGRLVGVYS 300
Qy 339 ACTVWLYSPESGEAFLELNPLOVEHPTTEMVSGVNIIPAOLQVAMGIPLYSRDRT 398
Db 301 ACTVWLYSHADKDFYFLELNPLOVEHPTTEGVSGVNLPAFASQLOIAMPILHRISDRL 360
Qy 399 LYGMPPRGNEVDIDFSSPESFKTKPOQGHVACRITANPTDTPKPGMGALTELNF 458
Db 361 LYGVDPKLSLTDIDFKPDPSEKTRORRSPKGLTACRITSDPGEKPGSVGMHLENF 420
Qy 459 RSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEARKOMVLSKELSGRDFRTTV 518
Db 421 RSSSNVWGYFSVGTGGIHSFSDSFQGHIFAYGENRSRKHVIALKELSGRDFRTTV 480
Qy 519 EYLKLETFEDNTITGWL DGLIQLDRLT 549

Db 481 EYLKLETFEDNTITGWLDELISKULT 511

RESULT 36

US-10-633-835-37
; Sequence 37, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 540
; TYPE: PRP
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(540)
; OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A
; OTHER INFORMATION: 42-581)
US-10-633-835-37

Query Match 70.3%; Score 2042.5; DB 4; Length 540;
Best Local Similarity 70.5%; Pred. No. 7.3e-176; Mismatches 82; Indels 3; Gaps 2;
Matches 380; Conservative 74; Mismatches 82; Indels 3; Gaps 2;

Qy 23 SPVADFTIRKGGHSHVITKVLICNNGIAAVERKIRKWAYETFGDERAIEFTVMATPDL 82
Db 3 SPLRDFVRSKHGGHSHVITKVLICNNGIAAVERKIRKWAYETFGDDRTVQVAVATPDL 62
Qy 83 KVNADYIRMDQYVEVPGSNNNNYANVDLIVDAERAGVAVWAGWGHASENRLPSL 142
Db 63 EANAERYIRMDQYIEVPGSTNNNNYANVDLIVDAERADVDVWAGWGHASENPLPEKL 122
Qy 143 AASKHKIIFIGPPGSAARSLGDKISSTIVAGHADVPKMPWSTGTIKETMMSDQ--GFLTV 200
Db 123 SQSKRKVIFIGPPGSAARSLGDKISSTIVAGHADVPKMPWSTGTIVVHVDKTLGLVSV 181
Qy 201 SDDVYQACIHTAEGLKAEKIGYPMIKASGGGGKIRKCTNGEEFKQLYNALVGEV 260
Db 182 DDDIYQGCCTSPEDGLOKAKRIGFPMIKASGGGGKIRKCTNGEEFKQLYNALVGEV 241
Qy 261 PGSPFVFMKLAGOARHLEVLQALLADQYGNALISIFGRDCSVORRHQKIIIEAPVTIAPEDAR 320
Db 242 PGSPFIMKLAGOARHLEVLQALLADQYGNALISIFGRDCSVORRHQKIIIEAPVTIAPEDAR 301
Qy 321 ESMEKAARLAKLVGVYSAGTVWLYSPESGEAFLELNPLOVEHPTTEMVSGVNIIPA 380
Db 302 HEMEKAARLAKLVGVYSAGTVWLYSPESGEAFLELNPLOVEHPTTEMVSGVNIIPA 361
Qy 381 QLOVAMGIPLYSRDITRLYGMPPRGNEVDIDFSSPESFKTKPOQGHVACRITAE 440
Db 362 QLOVAMGIPLYSRDITRLYGMPPRGNEVDIDFSSPESFKTKPOQGHVACRITAE 421
Qy 441 NPDTGKPGMGALTELNFRTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEARKQ 500
Db 422 DPNDGKPGMGALTELNFRTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSEARKQ 481
Qy 501 MVLISLKELSGRDFRTTVVEYLKLETFEDNTITGWL DGLIQLDRLTARPPADILAV 559
Db 482 MVLISLKELSGRDFRTTVVEYLKLETFEDNTITGWL DGLIQLDRLTARPPADILAV 540

RESULT 37

US-10-633-835-45
; Sequence 45, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633.835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(560)
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
; OTHER INFORMATION: domain (AAs 12-571)
US-10-633-835-45

Query Match 69.9%; Score 2033; DB 4; Length 560;
Best Local Similarity 69.2%; Pred. No. 5.6e-175;
Matches 380; Conservative 75; Mismatches 86; Indels 8; Gaps 3;

QY 3 PDHKAVSQFTGNNPLETAPASPVADFIKQGGHSHVTKVLCNNGIAAVKEIRKWAY 62
DB 18 PGH-----FGLNTVDKLEESPLRDFVKSHGGHTVSKILIANNGIAAVKEIRKWAY 72

QY 63 ETFGDERAIEFTVMATPEDLVNADYIRMAQVVEVPGGNNNNYANVDLIVDAERAGV 122
DB 73 ETFGDDRTVQFVAMATPEDLEANNAYIRMAQVIEVPGGNNNNYANVDLIVDAERADV 132

QY 123 HAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182
DB 133 DAVWAGHASENPLPEKLSQSKRVIFIGPPGNAMRSLGDKISSTIVAQAQKVPICPW 192

QY 183 SGTGKIKETWMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240
DB 193 SGTGV-DTVHVDEKTLVSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 251

QY 241 RKTNGEERKQLYNAVLGEVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 300
DB 252 ROVEREDFIALYHOANEIPGSPFIMKLAGARHLEVOLLADQYGTNLSLFRDCSVQ 311

QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNP 360
DB 312 RRHQKIIIEAPVTIAKETTHEMEKAAVRLKLVGYVSAGTVWLYSHDDGKVFLELNP 371

QY 361 RLOVEHPTTEMVSGVNPAAQLQVAMGIPLYSIRDITLYGMOPRGNEVIDFDFSSPESF 420
DB 372 RLOVEHPTTEMVSGVNLPAALQIANGIPMHRISDITLYGMNPHSASEIDFDFKTQDAT 431

QY 421 KTORKPOQGHVAVACRITAEENPDGFKPGMGALTELNFRSSTTWGYSFGTSGALHEYA 480
DB 432 KKORRPIPKGCHTACRITSDPDNDGFKPSGGTLHELNFRSSNNVWGYSFGNNGNTHSFS 491

QY 481 DSQFGHIFAYGADRSEARKOMVLSKELSGIRGDFRTTVEYLIKLETDAPESNKITTTGWL 540
DB 492 DSQFGHIFAFGENRQASRKHMVVALKELSGIRGDFRTTVEYLIKLETFEDFNITTTGWL 551

QY 541 DGLIQDRLT 549
DB 552 DDLITHKMT 560

RESULT 38

US-10-633-835-39
; Sequence 39, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633.835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(570)
; OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A
; OTHER INFORMATION: 2-571)
US-10-633-835-39

Query Match 69.9%; Score 2033; DB 4; Length 570;
Best Local Similarity 69.2%; Pred. No. 5.7e-175;
Matches 380; Conservative 75; Mismatches 86; Indels 8; Gaps 3;

QY 3 PDHKAVSQFTGNNPLETAPASPVADFIKQGGHSHVTKVLCNNGIAAVKEIRKWAY 62
DB 28 PGH-----FGLNTVDKLEESPLRDFVKSHGGHTVSKILIANNGIAAVKEIRKWAY 82

QY 63 ETFGDERAIEFTVMATPEDLVNADYIRMAQVVEVPGGNNNNYANVDLIVDAERAGV 122
DB 83 ETFGDDRTVQFVAMATPEDLEANNAYIRMAQVIEVPGGNNNNYANVDLIVDAERADV 142

QY 123 HAVWAGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPW 182
DB 143 DAVWAGHASENPLPEKLSQSKRVIFIGPPGNAMRSLGDKISSTIVAQAQKVPICPW 202

QY 183 SGTGKIKETWMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPVMIKASEGGGKGI 240
DB 203 SGTGV-DTVHVDEKTLVSVDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 261

QY 241 RKTNGEERKQLYNAVLGEVPGSPVFMKLAGARHLEVOLLADQYGNALISIFGRDCSVQ 300
DB 262 ROVEREDFIALYHOANEIPGSPFIMKLAGARHLEVOLLADQYGTNLSLFRDCSVQ 321

QY 301 RRHQKIIIEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVWLYSPESGEFAFLELNP 360
DB 322 RRHQKIIIEAPVTIAKETTHEMEKAAVRLKLVGYVSAGTVWLYSHDDGKVFLELNP 381

QY 361 RLOVEHPTTEMVSGVNPAAQLQVAMGIPLYSIRDITLYGMOPRGNEVIDFDFSSPESF 420
DB 382 RLOVEHPTTEMVSGVNLPAALQIANGIPMHRISDITLYGMNPHSASEIDFDFKTQDAT 441

QY 421 KTORKPOQGHVAVACRITAEENPDGFKPGMGALTELNFRSSTTWGYSFGTSGALHEYA 480
DB 442 KKORRPIPKGCHTACRITSDPDNDGFKPSGGTLHELNFRSSNNVWGYSFGNNGNTHSFS 501

QY 481 DSQFGHIFAYGADRSEARKOMVLSKELSGIRGDFRTTVEYLIKLETDAPESNKITTTGWL 540
DB 502 DSQFGHIFAFGENRQASRKHMVVALKELSGIRGDFRTTVEYLIKLETFEDFNITTTGWL 561

QY 541 DGLIQDRLT 549
DB 562 DDLITHKMT 570

RESULT 39
US-10-633-835-46
; Sequence 46, Application US/10633835
; Publication NO. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(550)
; OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
; OTHER INFORMATION: domain (AAS 17-566)
US-10-633-835-46

Query Match 69.7%; Score 2026; DB 4; Length 550;
Best Local Similarity 69.7%; Pred. No. 2.3e-174;
Matches 379; Conservative 73; Mismatches 84; Indels 8; Gaps 3;

Qy 3 PDHKAVSQFIGNPLETPASVADPIRQKQSHVITKVLNNGIAAVKEIRSIRKWAY 62
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 67

Qy 63 EFTGDERAIEFTVMTAPEDKYNADYIRMAOYVEVPVGSNNNNYANVDLIVDAERAGV 122
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 127

Qy 123 HAVWAGWGHASENPLPESLAASKHKIIFIGPPGAMRSLGDKISSTIVAHADVPCMPW 182
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 187

Qy 183 SGTGKETMMSDQ--GFLTVSDDVYQACIHTAEGLKAEKIGYPMVMIKASEGGGKGI 240
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 246

Qy 241 RKCTNGEFPKOLYNAVLEVPVGSPPVVMKLAGAARHLEVOLLADQYGNASIFGRDCSVQ 300
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 306

Qy 301 RRHQKIEEAPVTIAPEADARESMKAAVRLAKLVGVYSAGTVEMLYSPESGEFAFLELNP 360
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 366

Qy 361 RLOVEHPTEMVSGVNIIPAAQLQVANGIPLVSIIRDTLYGMDPRGNEVDFDSSPSFP 420
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 426

Qy 421 KTORQPOQGHVACRITAEINPDTGPKMGALTELNFERSSTTWGYSVGTSGALHEYA 480
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 486

Qy 481 DSQFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVYIYIKLLEDAFESNKITTGW 540
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 546

Qy 541 DGLI 544
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 550

Search completed: February 4, 2006, 18:28:37
Job time : 187 secs

RESULT 40
US-10-633-835-66
; Sequence 66, Application US/10633835
; Publication NO. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: N- and C-terminal deleted Magnaporthe ACCase BC domain (AAS
; OTHER INFORMATION: 72-572)
US-10-633-835-66

Query Match 69.5%; Score 2020; DB 4; Length 501;
Best Local Similarity 75.4%; Pred. No. 7.1e-174;
Matches 378; Conservative 54; Mismatches 69; Indels 0; Gaps 0;

Qy 39 TKULICNNGIAAIVEIRSIRKWAYETFGDERAIEFTVMTAPEDKYNADYIRMAOYVEV 98
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 60

Qy 99 PGSSNNNNYANVDLIVDAERAGVHVAWAGWGHASENPLPESLAASKHKIIFIGPPGSA 158
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 120

Qy 159 MRSIGDKISSTIVAHADVPCMPWSGTGKIKETMMSDQGLTVSDDVYQACIHTAEGL 218
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 180

Qy 219 KAEKIGYPMVMIKASEGGGKGIKCTNGEFPKOLYNAVLEVPVGSPPVVMKLAGAARH 278
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 240

Qy 279 VOLLADQYGNASIFGRDCSVQRRHQKIEEAPVTIAPEADARESMKAAVRLAKLVGVYS 338
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 300

Qy 339 AGTVEMLYSPESGEFAFLELNPRLQVEHPTEMVSGVNIIPAAQLQVANGIPLVSIIRDT 398
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 360

Qy 399 LYGMDDPRGNEVDFDSSPSFPKORQPOQGHVACRITAEINPDTGPKMGALTELNF 458
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 420

Qy 459 RSSSTTWGYSVGTSGALHEYADSOFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTV 518
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 480

Qy 519 EYIKLLEDAFESNKITTGW 539
Db .13 FGH-----FGLNTVDKLEESPLRFVKSHGHTVISKILIANNGIAAVKEIRSIRKWAY 501

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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:25:41 ; Search time 16 Seconds
(without alignments)
409.400 Million cell updates/sec

Title: US-10-633-835-2

Perfect score: 2907

Sequence: 1 PPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPADLAV 559

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1777.5	61.1	2455	7 US-11-186-999-14	Sequence 14, Appl
2	1777.5	61.1	2455	7 US-11-186-999-16	Sequence 16, Appl
3	1769.5	60.9	2256	7 US-11-144-368-4	Sequence 4, Appl
4	1769.5	60.9	2458	7 US-11-186-999-13	Sequence 13, Appl
5	1766.5	60.8	2458	7 US-11-186-999-6	Sequence 6, Appl
6	1739	59.8	2455	7 US-11-186-999-4	Sequence 4, Appl
7	1693.5	58.3	2458	7 US-11-186-999-11	Sequence 11, Appl
8	1673.5	57.6	2456	7 US-11-186-999-8	Sequence 8, Appl
9	1673.5	57.6	2456	7 US-11-186-999-10	Sequence 10, Appl
10	1669.5	57.4	2483	7 US-11-186-999-2	Sequence 2, Appl
11	1591.5	54.7	1096	6 US-10-995-561-710	Sequence 710, App
12	666	22.9	453	6 US-10-467-657-1642	Sequence 1642, Ap
13	640.5	22.0	703	6 US-10-821-234-1317	Sequence 1317, Ap
14	625	21.5	1151	6 US-10-793-626-2448	Sequence 2448, Ap
15	572	19.7	1124	6 US-10-858-730-12	Sequence 12, Appl
16	568	19.5	1127	6 US-10-858-730-13	Sequence 13, Appl
17	543.5	18.7	1140	6 US-10-858-730-208	Sequence 208, App
18	512.5	17.6	341	6 US-10-793-626-218	Sequence 218, App
19	508.5	17.5	453	6 US-10-793-626-804	Sequence 804, App
20	487	16.8	309	6 US-10-793-626-648	Sequence 648, App
21	178	6.1	1071	6 US-10-467-657-1654	Sequence 1654, Ap
22	167	5.7	1066	7 US-11-055-822-370	Sequence 370, App
23	167	5.7	1066	7 US-11-055-822-1002	Sequence 1002, Ap
24	167	5.7	1113	7 US-11-055-822-368	Sequence 368, App
25	167	5.7	1113	7 US-11-055-822-1000	Sequence 1000, Ap

Sequence 910, App
Sequence 3294, Ap
Sequence 1010, Ap
Sequence 9, Appli
Sequence 50, Appl
Sequence 3314, Ap
Sequence 8056, Ap
Sequence 316, App
Sequence 4, Appli
Sequence 5, Appli
Sequence 1146, Ap
Sequence 6, Appli
Sequence 18, Appli
Sequence 16, Appli
Sequence 7, Appli
Sequence 64, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 3280, Ap

ALIGNMENTS

RESULT 1
US-11-186-999-14
; Sequence 14, Application US/11186999
; Publication No. US20060019364A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
; FILE REFERENCE: BMS Docket Number 10245 NP
; CURRENT APPLICATION NUMBER: US/11/186,999
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 2455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-186-999-14

Query Match 61.1%; Score 1777.5; DB 7; Length 2455;
Best Local Similarity 63.4%; Pred. No. 2.5e-131;
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;
QY 22 ASPVADPIRQGGHSHVTKVLICNNGIAAVKETSIRKWAYETFGDERATEFTVMTAPED 81
DB 242 ASP-AEFVTRFGGNRVETVLIANNGLAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPD 300
QY 82 LKVNADYIRMDQYVEVPGSGNNNNYANVDLI DVDAERAGVHAWAGWGHASENPRLPES 141
DB 301 LKANAIEYKMDQYVVPVPGSGNNNNYANVELIIDIAKRIPVQAVWAGWGHASENPKLPEL 360
QY 142 LAASKHKIIFIGPGSGMSRLGDKISSTIVAHQADVPVMPWSGTGKETWMSD---QG-F 197
DB 361 LC--KHEIAFLGPPSEAMWALGDKISSTIVAQIPLPTLPWSGSLTVENTEDSQHGKC 418
QY 198 LTVSDVDYQOACHTAEGLKAEKIGYPMIKASGGGKGIRKCTNGEFKQLYNAV 257
DB 419 ISVPEDYEQGVDRVDEGLQAARVGFPLMIKASGGGKGIRRAESAEFDPLMFQVQ 478
QY 258 GEVPGSPFVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKITEEAPVTIAPE 317
DB 479 SEIPGSPFILMKLAQNAHLEVQVLADQYGNVSLFGRDCSIORRHQKITEEAPATIAAP 538
QY 318 DARESEKAARLAKULGVTVSAGTVEWLYSPSSGGEFAFELNPRLOVEHPTTMSGVNI 377
DB 539 AVPEFMEQCAVLAKTVGVVSAGTVEYLYS-ODGSPHFLELNPRLQVEHPCTEMADVNL 597
QY 378 PAAQLQVANGIPLYSTRDIRTLTYGMDPRGNEVIDDFSSPSEPKTKQKQ-PQGHVACR 436

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Db 598 PAAQLQIANGVPLHRLKDRLLYGSPWG-----VTPVSFETPLSPPIARGHVIAAR 649
Qy 437 ITAENPDGFKPGMGALTELNFRSSTWGYFSGVTSGALHEYADSQFCHIFAYGADRSE 496
Db 650 ITSENPDGFKPSSGTVOELNFRSNKNVWGYFSAAGLHEFAFADSGHCFSGENREE 709
Qy 497 ARKQWVLSKELSIKSGDRTTVEYLILKLETDAPESNKITTGWLDGLIQDRLTAERPPAD 556
Db 710 AISNMVVALKELSIKSGDRTTVEYLILNLETESFQNDIDTGWLDHLIAQVQAEKPDIM 769
Qy 557 LAV 559
Db 770 LGV 772

RESULT 2
US-11-186-999-16
; Sequence 16, Application US/11186999
; Publication No. US200600193641
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
; FILE REFERENCE: BMS Docket Number 10245 NP
; CURRENT APPLICATION NUMBER: US/11/186,999
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 2455
; ORGANISM: Rattus norvegicus
US-11-186-999-16

Query Match 61.1%; Score 1777.5; DB 7; Length 2455;
Best Local Similarity 63.4%; Pred. No. 2.5e-131;
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;

Qy 22 ASPVADPFRKOGGHSVITKVLICNNGIAAVKEIRSIKWAYETFGDERAIEFTVMATPED 81
Db 242 ASP-AEFVTRFGGNRVITVLIANNGIAAVKCMRSIRRAWEMPRNERAIRFVVMVTPED 300
Qy 82 LKNVADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHGHASENPRLPES 141
Db 301 LKANAERYIKMADQYVPGGPNNNYANVELIIDIAKIPVQAVWAGHGHASENPKLP 360
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQADVPKMPWSTGTGKIKETWMSD--QG-F 197
Db 361 LC--KHEIAFLGPPSEAMWALGDKISSTIVAQTLQIPTLPWSSGLTVEWTEDSHQGKC 418
Qy 198 LTVSDVYQOACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEERFKOLYNV 257
Db 419 ISVPEDVYQOQVRDDEGLQAAEKYGFPLMIKASEGGGKGIRRAESAEDFPMLFRQVQ 478
Qy 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNVLSIFGRDCSVORRHQKIEEAPVTIAPE 317
Db 479 SEIPGSPIFLMKLAQARHLEVQLADQYGNVLSIFGRDCSVORRHQKIEEAPVTIAAP 538
Qy 318 DARESMEKAAVRLAKLVGYVSAGTVWLYSPESGSEFAPLELNPRLOVEHPHPTTEMVSGVNI 377
Db 539 AVFEPMEQCAVLAKTVGVVSAGTVWLYS-ODGSFHFLELNPRLOVEHPHPTTEMV 597
Qy 378 PAAQLQVANGPIYSIRDIRTYLGMDDPRGNEVIDFDFSSPSFKTORQPO-POGHVACR 436
Db 598 PAAQLQIANGVPLHRLKDRLLYGSPWG-----VTPVSFETPLSPPIARGHVIAAR 649
Qy 437 ITAENPDGFKPGMGALTELNFRSSTWGYFSGVTSGALHEYADSQFCHIFAYGADRSE 496
Db 650 ITSENPDGFKPSSGTVOELNFRSNKNVWGYFSAAGLHEFAFADSGHCFSGENREE 709
Qy 497 ARKQWVLSKELSIKSGDRTTVEYLILKLETDAPESNKITTGWLDGLIQDRLTAERPPAD 556
Db 710 AISNMVVALKELSIKSGDRTTVEYLILNLETESFQNDIDTGWLDHLIAQVQAEKPDIM 769
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Qy 557 LAV 559
Db 770 LGV 772

RESULT 3
US-11-144-368-4
; Sequence 4, Application US/11144368
; Publication No. US20050272082A1
; GENERAL INFORMATION:
; APPLICANT: Kan, Zhengyan
; APPLICANT: Garrett-Engle, Philip W.
; APPLICANT: Armour, Christopher D.
; APPLICANT: Raymond, Christopher K.
; APPLICANT: Castle, John C.
; TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORM OF
; FILE REFERENCE: ACETYL-COA CARBOXYLASE 2 (ACC2)
; CURRENT APPLICATION NUMBER: US/11/144,368
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,234
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-368-4

Query Match 60.9%; Score 1769.5; DB 7; Length 2256;
Best Local Similarity 63.4%; Pred. No. 9.6e-131;
Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;

Qy 22 ASPVADPFRKOGGHSVITKVLICNNGIAAVKEIRSIKWAYETFGDERAIEFTVMATPED 81
Db 43 ASP-AEFVTRFGGDRVIEKVLIANNGIAAVKCMRSIRRAWEMPRNERAIRFVVMVTPED 101
Qy 82 LKNVADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHVAWAGHGHASENPRLPES 141
Db 102 LKANAERYIKMADYVVPVPGGPNNNYANVELIIDIAKIPVQAVWAGHGHASENPKLP 161
Qy 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQADVPKMPWSTGTGKIKETWMSD--QG-F 197
Db 162 LC--KNGVAFGLPSPSEAMWALGDKIASTVVAQTLQVPTLPWSSGLTVEWTEDDLOQQR 219
Qy 198 LTVSDVYQOACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGEERFKOLYNV 257
Db 220 ISVPEDVYQGVKVDVDEGLEAAERIGFPLMIKASEGGGKGIRKAESAEDFPILFRQVQ 279
Qy 258 GEVPGSPVFMKLAGQARHLEVQLLADQYGNVLSIFGRDCSVORRHQKIEEAPVTIAPE 317
Db 280 SEIPGSPIFLMKLAQARHLEVQLADQYGNVLSIFGRDCSVORRHQKIEEAPVTIAPL 339
Qy 318 DARESMEKAAVRLAKLVGYVSAGTVWLYSPESGSEFAPLELNPRLOVEHPHPTTEMVSGVNI 377
Db 340 AITEFMEQCAIRLAKTVGVVSAGTVWLYS-ODGSFHFLELNPRLOVEHPHPTTEMV 398
Qy 378 PAAQLQVANGPIYSIRDIRTYLGMDDPRGNEVIDFDFSSPSFKT-ORKPOQGHVACR 436
Db 399 PAAQLQIANGVPLHRLKDRLLYGSPWG-----VTPISFETPSNPPLARGHVIAAR 450
Qy 437 ITAENPDGFKPGMGALTELNFRSSTWGYFSGVTSGALHEYADSQFCHIFAYGADRSE 496
Db 451 ITSENPDGFKPSSGTVOELNFRSNKNVWGYFSAAGLHEFAFADSGHCFSGENREE 510
Qy 497 ARKQWVLSKELSIKSGDRTTVEYLILKLETDAPESNKITTGWLDGLIQDRLTAERPPAD 556
Db 511 AISNMVVALKELSIKSGDRTTVEYLILNLETESFQNDIDTGWLDHLIAQVQAEKPDIM 570
Qy 557 LAV 559
Db 571 LGV 573
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Query Match 59.8%; Score 1739; DB 7; Length 2455;
Best Local Similarity 62.8%; Pred. No. 2.7e-128;
Matches 341; Conservative 75; Mismatches 107; Indels 20; Gaps 8;

QY 22 ASPVADPIKOGGSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 81
DB 245 ASP-AEFVTRFGGDRVIEKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 303
QY 82 LKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPES 141
DB 304 LKANAETIKWADHYVPVPGGNNNNYANVELIVDIKRI PVKAXWXXXHASENPKLP 363
QY 142 LAASKHKIIFIGPPGSAKSLGDKISSTIVAHADVPCMPWSTGIGKEMTMSD---QG-F 197
DB 361 LC--KNGVAFGLPSPSEAMWALGDKIASTVVAQTLOVPTLPWSSGLTVWETDDLOQGR 418
QY 198 LTVSDVYQOACIHTAEGLKAEKIGYPMVKASSEGKGGKIRKCTNGEFPKQLYNAV 257
DB 419 ISVPEDVYDKGVDEGLEAERIGFPLMKASSEGKGGKIRKASAEADFPILFRQVQ 478
QY 258 GEVPGSPVFMKLAGOARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAP 317
DB 479 SEIPGSPIFLMKLAQHARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAP 538
QY 318 DARESEKAAVRLAKLVGYSAGTVWELVSPSEGEPAFLNPRLOVEHPTTEMVSGVNI 377
DB 539 AIFEFMEQCAIRLAKTVGYSAGTVWELVSPSEGEPAFLNPRLOVEHPTTEMVSGVNI 597
QY 378 PAAQLQVAMGIPLYSIRDIRTLGMDPRGNEVIDDFSSPESFKT-ORKPOQGHVACR 436
DB 598 PAAQLQVAMGIPLYSIRDIRTLGMDPRGNEVIDDFSSPESFKT-ORKPOQGHVACR 649
QY 437 ITAENPDTGPKPMGALTELNFRSSTSTWGYFSGVTSGLALHEYADSQFGHIFAYGADRSE 496
DB 650 ITSENPEDEGKPSGGTVQELNFRSSKNVGYFSAATGGLHEFADSQFGHCFSGWENREE 709
QY 497 ARKQWISLKELSIRGDFRTTVEYLKLETDAFESNKITTWGLDGLDRLTAERPPAD 556
DB 710 AISNMVVALKELSIKRGDFRTTVEYLKLETDAFESNKITTWGLDGLDRLTAERPPAD 769
QY 557 LAV 559
DB 770 LGV 772

RESULT 7
US-11-186-999-11
; Sequence 11, Application US/11186999
; Publication No. US20060019364A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
; FILE REFERENCE: BMS Docket Number 10245 NP
; CURRENT APPLICATION NUMBER: US/11/186,999
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 2458
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(2458)
; OTHER INFORMATION: Xaa is any amino acid
US-11-186-999-11

Query Match 58.3%; Score 1693.5; DB 7; Length 2458;
Best Local Similarity 61.3%; Pred. No. 1e-124;
Matches 333; Conservative 74; Mismatches 119; Indels 17; Gaps 7;

QY 22 ASPVADPIKOGGSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 81
DB 245 ASP-AEFVTRFGGDRVIEKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 303
QY 82 LKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPES 141
DB 304 LKANAETIKWADHYVPVPGGNNNNYANVELIVDIKRI PVKAXWXXXHASENPKLP 363
QY 142 LAASKHKIIFIGPPGSAKSLGDKISSTIVAHADVPCMPWSTGIGKEMTMSD---QG-F 197
DB 361 LC--KNGVAFGLPSPSEAMWALGDKIASTVVAQTLOVPTLPWSSGLTVWETDDLOQGR 418
QY 198 LTVSDVYQOACIHTAEGLKAEKIGYPMVKASSEGKGGKIRKCTNGEFPKQLYNAV 257
DB 419 ISVPEDVYDKGVDEGLEAERIGFPLMKASSEGKGGKIRKASAEADFPILFRQVQ 478
QY 258 GEVPGSPVFMKLAGOARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAP 317
DB 479 SEIPGSPIFLMKLAQHARHLEVQLLADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAP 538
QY 318 DARESEKAAVRLAKLVGYSAGTVWELVSPSEGEPAFLNPRLOVEHPTTEMVSGVNI 377
DB 539 AIFEFMEQCAIRLAKTVGYSAGTVWELVSPSEGEPAFLNPRLOVEHPTTEMVSGVNI 597
QY 378 PAAQLQVAMGIPLYSIRDIRTLGMDPRGNEVIDDFSSPESFKT-ORKPOQGHVACR 436
DB 598 PAAQLQVAMGIPLYSIRDIRTLGMDPRGNEVIDDFSSPESFKT-ORKPOQGHVACR 649
QY 437 ITAENPDTGPKPMGALTELNFRSSTSTWGYFSGVTSGLALHEYADSQFGHIFAYGADRSE 496
DB 650 ITSENPEDEGKPSGGTVQELNFRSSKNVGYFSAATGGLHEFADSQFGHCFSGWENREE 709
QY 497 ARKQWISLKELSIRGDFRTTVEYLKLETDAFESNKITTWGLDGLDRLTAERPPAD 556
DB 710 AISNMVVALKELSIKRGDFRTTVEYLKLETDAFESNKITTWGLDGLDRLTAERPPAD 769
QY 557 LAV 559
DB 770 LGV 772

RESULT 8
US-11-186-999-8
; Sequence 8, Application US/11186999
; Publication No. US20060019364A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
; FILE REFERENCE: BMS Docket Number 10245 NP
; CURRENT APPLICATION NUMBER: US/11/186,999
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 2456
; TYPE: PPT
; ORGANISM: Rattus norvegicus
US-11-186-999-8

Query Match 57.6%; Score 1673.5; DB 7; Length 2456;
Best Local Similarity 60.2%; Pred. No. 3.9e-123;
Matches 327; Conservative 78; Mismatches 121; Indels 17; Gaps 7;

QY 22 ASPVADPIKOGGSHVITKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 81
DB 241 ASP-AEFVTRFGGDRVIEKVLICNNGIAAIVKESIRKWAYETFGDERAIEFTVWATPDED 299
QY 82 LKVNADYIRMDQYVEVPGGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPES 141
DB 300 LKANAETIKWADHYVPVPGGNNNNYANVELIVDIKRI PVKAXWXXXHASENPKLP 359
QY 142 LAASKHKIIFIGPPGSAKSLGDKISSTIVAHADVPCMPWSTGIGKEMTMSD---QG-F 197
DB 360 LC--KNGVAFGLPSPSEAMWALGDKIASTVVAQTLOVPTLPWSSGLTVWETDDLOQGR 417
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QY 497 ARKQWISLKELSGRDPRTTVEYLKLETDAPESNKITTWGLDGLIQRDLTAERPPAD 556
DB 713 AISNMVVALKELSLGRDPRTTVEYLINLLETESFQNNYIDTGWLDYLAERKQ-QKPNIM 771
QY 557 LAV 559
DB 772 LGV 774

RESULT 11
US-10-995-561-710
; Sequence 710, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710
; LENGTH: 1096
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-710

Query Match 54.7%; Score 1591.5; DB 6; Length 1096;
Best Local Similarity 58.1%; Pred. No. 3.3e-117;
Matches 315; Conservative 65; Mismatches 93; Indels 69; Gaps 6;

QY 22 ASPVADFIKOGGSHVITKVLICNNGIAAVKSIKWAYETFGDERAIEFTVMATPED 81
DB 245 ASP-AEFTVTRFGGDRVIEKVLIANNGIAAVKMSIRWAYEMFRNRAIRFVVMVTPED 303
QY 82 LKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVAVVAGWGHASENRLPES 141
DB 304 LKANAERYIKMADHYVPVPGSGNNNNYANVELIVDAKRIFFVQAVVAGWGHASENKLPEL 363
QY 142 LAASKHKLIFIGPGSAMESLGDKTSSTIVAGHADVPWCPWSTGTGKETMMSD--QG-F 197
DB 364 LC--KNGVAFPPPEAMWALGDKTASTVVAOTLQVTLFWSGSGUTVETWEDDLQOQKR 421
QY 198 LTVSDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQLYNVL 257
DB 422 ISVPEDVDKGVKVDDEGLEAAERIGFPLMIKASEGGGKGIKKAESAEDFPILFRQVQ 481
QY 258 GEVPGSPVFMKLAGQARHLEVOLLADQYGNALISIFGRDCSVORRHOKIIEBAPVTIAPE 317
DB 482 SEIPGSPIFLMKLAQHARHLEVQILADQYGNVSLFGRDCSVORRHOKIIEBAPVTIAPE 541
QY 318 DARSEKAAVRLAKLVGVVSAGTVEMWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
DB 542 AIFEFMEQCAIRLAKTVGVVSAGTVEMWLYS-QDGSFHFLELNPRLQVEHPTTEMVADNVL 600
QY 378 PAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFSSPESFKTQKPPQPOGHVACRI 437
DB 601 PAAQLQ----- 606
QY 438 TAENPDTPGKPGMGALTENFRSSTSTWGYFSVGTSGALHEVADSQFGHIIPAYGADRSEA 497
DB 607 -----GPKPSGTVQELNFRSSKNWGYFSVAATGGLHFADSQFGHCFSGWGNRBEA 659
QY 498 RKQWISLKELSGRDPRTTVEYLKLETDAPESNKITTWGLDGLIQRDLTAERPPADL 557
DB 660 ISNMVVALKELSGRDPRTTVEYLINLLETESFQNNYIDTGWLDYLAERKQVQAEKPDIML 719
QY 558 AV 559
DB 720 GV 721
```

RESULT 12

US-10-467-657-1642
; Sequence 1642, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1642
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1642

Query Match 22.9%; Score 566; DB 6; Length 453;

Best Local Similarity 31.9%; Pred. No. 5.7e-45;
Matches 168; Conservative 92; Mismatches 180; Indels 86; Gaps 13;

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QY 37 VITKVLICNNGIAAVKSIKWAYETFGDERAIEFTVMATPEDLKNADYIRMAQYV 96
DB 1 MLKVLINRGEIARVLRACRENGIAT-----VAHSETDKSLHVKLADRSV 49
QY 97 EVPGSGNNNNYANVDLIVDAERAGVAVVAGWGHASENRLPESLAASKHKLIFIGPPG 156
DB 50 CIGPAASAQSYLNIPATIAAAEVTCADAVHPGYGFLAENADFAEQVEQS--GFTFIGPKP 107
QY 157 SAMESLGDKTSSTIVAGHADVPWCPWSTGTGKETMMSDQGLTVDVYQQACIHTABEG 216
DB 108 DTIRLMGDKVSAMKAMTAAGVPCVPGSDGALPD-----DDA-----EI 145
QY 217 LEKAEKIGYPVMIKASEGGGKGIKCTNGEEFKQ---LYNAVLGVEVPGSP-VFVKLAG 272
DB 146 LKIDAKVGPVILIKASGGGGRGVVVEKEDDLQSVEMTKAEAGAAFGNPMVYMERVLQ 205
QY 273 QARHLEVOLLADQYGNALISIFGRDCSVORRHOKIIEBAPVTIAPEDARESMEKAARLAK 332
DB 206 RPRHVEIQVLADERHNAVYLAERDCSLQRRHOKVIEEAPAPFIDEKARKKIGKACTDACK 265
QY 333 LVGVVSAGTVEMWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIIPAAQLQVAMGIP 391
DB 266 RIGYRGAGTFFELY--EDGEFFTEMNTRVQVEHPTTELITGVDIVQQLRIASGLPLQY 323
QY 392 SIRDITLYGMDPRGNEVIDFSSPESFKTQKPPQPOGHVACRI TAENPDTPGKPGMG 451
DB 324 KQDIKI-----EGHAFECRINAEDP--YNIIPSPG 352
QY 452 ALTELNFRSSTSTWGYFSVGTSGALHE-----YADSQFGHIIPAYGADRSEARKQWISL 505
DB 353 PI-----ESCHLPGGFGIRVDSHIYQYRPPYVDSLIGKICVHGKTRREQMAKQVRL 406
QY 506 KELSIRGDFRTTVEYLKLETDAPESNKITTWGLDGLIQRDLTAEL 551
DB 407 AELAVTG-IKTNTPLHRDLDFADAGFQEGGVSIHYLHLEHWLEARKTKQ 451
```

RESULT 13

US-10-821-234-1317
; Sequence 1317, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit


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; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1317
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1317

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Query Match	22.0%	Score 640.5	DB 6	Length 703
Best Local Similarity	31.8%	Pred. No. 1.le-42		
Matches 166	Conservative 87	Mismatches 176	Indels 91	Gaps 12
Qy	40	KVLICNNGIANVKEIRSIRKWAYETFGDERALIEFTVMATPEDLKNADYIRMAQYVEVP	99	
Db	40	KILVANRGEIACRVIRTKONGIKT-----VAIHSDVDASSVHVWMADEAVCVG	88	
Qy	100	GGSNNNYANVDLVDVAERAGVHAVWAGWGHASENRPELPSLAAASKHKIIFIGPPGSAM	159	
Db	89	PAPTSKSVLNNDALMEAIKKTQAQAVHPGYGFLSENKEFARCLAA--EDVVFIGPDTHAI	146	
Qy	160	RLSGDKISSTTIAQHADVCPMPWSGTGIKETMMSDQGFLLTVSDVDYQOACIHTAEGLEK	219	
Db	147	QAMGDKIESKLLAKAEVNTIP-----GFDGVVKD-----AEEAVRI	183	
Qy	220	AELIGYPWMIKASGGGGKGRKCTNGEEFKQLYNAVILGEVPGS----PVFVWKLACQAR	275	
Db	184	ARELIGYPWMIKASGGGGKGRMIANDDEETRDGFRLLSQEAASFGDDRLLIIEKFIDNPR	243	
Qy	276	HLEVQLLADQYGNIAISIFGRDCSVQRBRHQKIEEAPVTIAPEDARESMKAAVRLAKLVG	335	
Db	244	HIEIQVLGDGHGNALWLNRECSIQRRNQKVVEAPSIFLDAETTRAMGQAVALARAVK	303	
Qy	336	YVSAGITVEWLYSPESGGEFAFLNPNRLQVHPHTTEMVSGVNIIPAQLQVAMGIPL-VYSIR	394	
Db	304	YSSAGITVEFLVDSSK-NFYFLEMNTRLQVHPVPTCEITGLDLVQEMIRVARGYPLRHKQA	362	
Qy	395	DIRTLYGMDPRGNEVIDDFDSSPESFKTRKQPQGHVACRIATAENPDTFG-KPGNGAL	453	
Db	363	DIRI-----NGWAVECRVVAEDPYKSGFLPSIGRL	392	
Qy	454	TE-----LNFRSSTTWGVSFGTSGALHEYADSOFCHEIFAYGADRSEARKONVIS	504	
Db	393	SOYQEPHLHPGVVRDVGSIQPGSDISI-----YYDPMISKLITYGSDRTEALKRWADA	444	
Qy	505	LKELSRIGDRFTTVEYLKILETDAFPESNKITTCWGLDGLIQD	546	
Db	445	LDNVIYRG-VTHNIALLRVIINSRFVKYGDISTKFLSDVYPD	485	

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RESULT 14
US-10-793-626-2448
; Sequence 2448, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2448
; LENGTH: 1151

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2448

Query Match      21.5%; Score 625; DB 6; Length 1151;
Best Local Similarity 31.8%; Pred.No.3.7e-41;
Matches 164; Conservative 91; Mismatches 182; Indels 78; Gaps 14

QY 38 ITKVLICNNGIAAWEKRSIRKWAYETFGDERALEFTVMATPEDLKYNADYIRMADQYVE 97
Db 8 IKLLVANRGEIAIRIFRA-----AAELNISTVAIYSNED-KSLHRYKADESYLV 57

QY 98 VPGSSNNNTYANDVLIYDVAAERAGVHVAWGWHGASHENRPLPESLAASKHKHIIIFGPPGS 157
Db 58 GSDLGPAESYLNRIIEVALRAGVDIAHPGYGLSENEQFARCA--EGIKFIQHPLE 115

QY 158 AMRSLGDKISSTIVAAHADVPCHWMSGTGIKETWMSDQGLFTVSDDYVQQAQCIHTABEGL 217
Db 116 HLMDFGDKVKARTTAINANLPVIP--GT-----DGPISFEAAE 152

QY 218 EKAETGYPWIKASGGGGKGIRKCTNGEEFKOLYNVLGEVP----GSPVFMWKLQG 273
Db 153 QFANEAGYPLMIKATSGGGGKGWRIVRESSELEDAPFRHAKSEAKSFGNSEVYIERIDN 212

QY 274 ARHLEVQLLADQYGNASIFGRDCSVORRHQKIIIEEAPVTIAPEDARESMEKAARVLAKL 333
Db 213 PKHIEVQVIGDFEGNIHLHYERDCSVORRHQKVVEVAPSVGLSNKLEERICDAAIQLMEN 272

QY 334 VGYVSAGTVEWLYSPSEGEPAFLELNPRLQVEHTPTMVGSGVNIIPAAQLQVAMGIPLYSI 393
Db 273 IKYVNAQTVEFLVSGD--EFFFTIEVNPVQVEHTITEMITGIDIVKTQILVADGESLP-- 328

QY 394 RDILTYLGMDPRCNEVIDPDFSSEPFKTKRQPOGHVVACRITANPDTKGPGMGAL 453
Db 329 -----GDKL-----SMPQNEYQLTGIAIQCRITTEDPDYNDNMPDSG-- 365

QY 454 TELNFRSSTWTGYSFV-----GTSGA--LHEYADSQFGHIFAYGADRSEARKQMWISLK 506
Db 366 TIITAYRSS---GGFGVRLDAGDGFQGAETSPYDLSLLVKLSLTHAVSPKQAEKWEKSLR 421

QY 507 ELSIRGDFPTTVEYLIKLETPAESNKITTTGWL D 541
Db 422 EMRIIG-VKTNIPFLINVMNDRKFRSGDYTTKFE 455

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RESULT 15
US-10-858-730-12
; Sequence 12, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730.
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 1124
 TYPE: PRT
 ORGANISM: Streptomyces coelicolor
 US-10-858-730-12

Query Match 19.7%; Score 572; DB 6; Length 1124;
 Best Local Similarity 30.8%; Pred. No. 5.3e-37;
 Matches 161; Conservative 87; Mismatches 199; Indels 76; Gaps 14;

QY 40 KVLICNNGIAAAYKKEIRSIKWAYETEGDERAIEFTVMATPEDLKNADYIRMADQVVEVP 99
 DB 4 KVLVANRGIAIRAFRA-----GVK-LGAR-----TVAVFPHEDRNSLHRLKADAEYETGE 53

QY 100 GGSNNNNYANVDLIYDVAERAGVHAYWAGMGHASENPRLPESLAASKHKIIFIGPPGSAM 159
 DB 54 QGHPVRAYLSVEEIVRAARRAGADAVYPGYGFLENPEL--ARACEEAGITFVGPSARIL 111

QY 160 RSLGDKISSTIVQAHDVPCMPWSGTGKETWMSDQGLTVSDVYQOACIHTAEGLK 219
 DB 112 ELTGKARAVAAAREAGVPL-----GSSAPSTDV-----DELVRA 147

QY 220 ASKIGVPMIKASEGGGKIRKCTNGEERFKOLYNVILGEVPG-----SPVFMKLAGOAR 275
 DB 148 ADVGFPVFKAVAGGGGGRMRVEPAQIREAIEAASREASAFGDSITVFLEKAVVEPR 207

QY 276 HLEVOLLADQYGNALISIFGRDCSVQRRHQIIEEAPVTIAPEDARESMKAAVRLAKLVG 335
 DB 208 HIEVQILADGEGDVHILFERDCSVQRRHQVIELAPAPNLDPALRERICADAVNFAHQIG 267

QY 336 YVSGTVEWLYSPESGEFAFLEINPRLOVHEHTTEMVSGVNTPAALQVAMGIPLYSIRD 395
 DB 268 YRNAGTVEPLVD-RDGNHVFIEENPRIQVEHTVTEETVDVLSQSLRIAAAGTILADL-- 324

QY 396 INTLYSGMDPRGNEVDIFDSSPESFKTORQPQGHVACRITAENPDGFKPGMGALTE 455
 DB 325 -----GL-----AQENITLRGAALOCRITTEDPANGFPDGTGQISA 360

QY 456 LNFIRSTSTWGYFSVGTSGA---LHEYADSQGHIFAYGADRSEARKQWISLKELSI 512
 DB 361 --YRSPGGGIRLDGCTHAGTEISAHFDLSMLVKLSRGRDFTTAVNRRARRAVERFRIG 418

QY 513 DFRITVEYLIKLETDAPESNKITGWLD---GLIQDRLTAER 552
 DB 419 -VATNIPFLQAVLDLDPDFQAGRVTTTSFIEQRPHLLTAHRSADR 460

RESULT 16
 US-10-858-730-13
 Sequence 13, Application US/10858730
 Publication No. US20050255568A1
 GENERAL INFORMATION:
 APPLICANT: Bailey, Richard B.
 APPLICANT: Blomquist, Paul
 APPLICANT: Doten, Reed
 APPLICANT: Driggers, Edward M.
 APPLICANT: Madden, Kevin T.
 APPLICANT: O'Leary, Jessica
 APPLICANT: O'Toole, George
 APPLICANT: Trueheart, Joshua
 APPLICANT: Walbridge, Michael J.
 APPLICANT: Yorgey, Peter S.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
 FILE REFERENCE: 14184-030001
 CURRENT APPLICATION NUMBER: US/10/858,730
 CURRENT FILING DATE: 2004-06-01
 PRIOR APPLICATION NUMBER: US 60/475,000
 PRIOR FILING DATE: 2003-05-30
 PRIOR APPLICATION NUMBER: US 60/551,860
 PRIOR FILING DATE: 2004-03-10
 NUMBER OF SEQ ID NOS: 364

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 1127
 TYPE: PRT
 ORGANISM: Mycobacterium smegmatis
 US-10-858-730-13

Query Match 19.5%; Score 568; DB 6; Length 1127;
 Best Local Similarity 30.5%; Pred. No. 1.1e-36;
 Matches 162; Conservative 88; Mismatches 196; Indels 86; Gaps 16;

QY 37 VITKVICNNGIAAAYKKEIRSIKWAYETEGDERAIEFTVMATPED-----LKNVADYIR 90
 DB 1 MISKVLNVRGIAIRAFRA-----AY-----EMGIATVAVPYEDRNSLHRLKADASY-- 49

QY 91 MADQYVEYVPGSGNNNNYANVDLIYDVAERAGVHAYWAGMGHASENPRLPESLAASKHKI 150
 DB 50 --QIGEV--GHPVRAYLSVEEIVRAARRAGADAVYPGYGFLENPEL--LAACKCAEA--GIT 102

QY 151 FIGPPGSAMRSLGDKISSTIVQAHDVPCMPWSGTGKETWMSDQGLTVSDVYQOACI 210
 DB 103 FVGPFAEVLQITGNKARAIAAARAAGLPVLSSEPS----- 138

QY 211 HTAEGLKAEKIGVPMIKASEGGGKIRKCTNGEERFKOLYNVILGEVPG-----SPVF 266
 DB 139 SSVDELMAAADMEFFLVKAVSGGGGGRMRVTDRESLAIEAASREASAFGDASY 198

QY 267 VMKLAGOARHLEVOLLADQYGNALISIFGRDCSVQRRHQIIEEAPVTIAPEDARESMK 326
 DB 199 LEQAVLNPRIHIEVQILADGAGNVMLPERDCSVQRRHQVVELAPAPNLSDELROQICAD 258

QY 327 AVRLAKLVGYVSAGTVEWLYSPESGEFAFLEINPRLOVHEHTTEMVSGVNTPAALQVAM 386
 DB 259 AVAFARQIGYSCAGTVEFLD-ERGHVFIENPRIQVEHTVTEETVDVLSQSLRIAA 317

QY 387 GIPLYSIRDINTLYSGMDPRGNEVDIFDSSPESFKTORQPQGHVACRITAENPDGTF 446
 DB 318 GETLADL-----GL-----SQDLVVRGAMQCRITTEVPANGF 351

QY 447 KPGMGALTELNFRSSTWGYFSVGTSGA-LHEYADSQGHIFAYGADRSEARKQWIS 504
 DB 352 RPDGTGRITA--YRSPGGGIRLDGCTHAGTEISAHFDLSMLVKLTGCRDRFSAASARRA 409

QY 505 LKELSIKELSDFRITVEYLIKLETDAPESNKITGWLDGLIQDRLTAERPPAD 556
 DB 410 LAEPRIRG-VSTNIPFLQAVLDLDPDFQAGRVTTTSFIDD--RPHLLTSRSPAD 458

RESULT 17
 US-10-858-730-208
 Sequence 208, Application US/10858730
 Publication No. US20050255568A1
 GENERAL INFORMATION:
 APPLICANT: Bailey, Richard B.
 APPLICANT: Blomquist, Paul
 APPLICANT: Doten, Reed
 APPLICANT: Driggers, Edward M.
 APPLICANT: Madden, Kevin T.
 APPLICANT: O'Leary, Jessica
 APPLICANT: O'Toole, George
 APPLICANT: Trueheart, Joshua
 APPLICANT: Walbridge, Michael J.
 APPLICANT: Yorgey, Peter S.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
 FILE REFERENCE: 14184-030001
 CURRENT APPLICATION NUMBER: US/10/858,730
 CURRENT FILING DATE: 2004-06-01
 PRIOR APPLICATION NUMBER: US 60/475,000
 PRIOR FILING DATE: 2003-05-30
 PRIOR APPLICATION NUMBER: US 60/551,860
 PRIOR FILING DATE: 2004-03-10
 NUMBER OF SEQ ID NOS: 364

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-858-730-208

Query Match 18.7%; Score 543.5; DB 6; Length 1140;
Best Local Similarity 29.3%; Pred. No. 9.5e-35;
Matches 157; Conservative 90; Mismatches 188; Indels 101; Gaps 16;

QY 40 KVLICNNGIAAWEIRSIKWAYETFCGERAIEFTVMATPEDLKNVADYIRMDQVVEV- 98
DB 14 KILVANGETAVRAFA-----ALETGA-----ATVAIYPREDR-GSFHRSFASAVRIG 62

QY 99 PGGSNNNNYANVDLIVDAERAGVHVAWGWHASENPRIPESLAASKHKIIFIGPPGSA 158
DB 63 TEGSPVKAYLIDIBIIGAANKKADAIYPGYGLSENAQLARECA--ENGITFIGTPEV 120

QY 159 MRSGLDKISSTIVAHQADVPCMPWSGTGKETMMSDQGLTVSDDDVYQQACIHTAEGL 218
DB 121 LDLTGDKSAVTAACKAGLPLAES-----TPSKNI-----DEIVK 156

QY 219 KAEKIGYPMIKASGGGGKIGKCTNGBEFKOLYNALVGEVPGS-----PVFVMKLAGQA 274
DB 157 SAGQTYPIPVKAVAGGGGGMFVAPDELRLKLAATESREAAAFGDBGAVYVERAVINP 216

QY 275 RHLEVOALLDQYGNVAISIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEKAVALKLIV 334
DB 217 OHIEVOILGDHTEVHLVERDCSLORRQKQVVEIAPAOHLDELDRICADAVKFRSI 276

QY 335 GYVSAGTVEWLYSPSEGEFAFLNRLQVEHPHTTMSVGNIPAAQLQVAMGIPLYSIR 394
DB 277 GYQAGTVEFLVD-EGKNHVFIEMNPRIQVEHTVTVEEVDLVKAQMLAAGATLKEI- 334

QY 395 DIRTLYGMDPRGNEVIDDFSSPESKTORKPOQGHVACRITAENPDTPGKPGMGALT 454
DB 335 -----GL-----TQDKIKTHGAALQCRITTEDPNNGFRPDTGTIT 369

QY 455 ELNFRSSTWGSYVSGTSGALHEYADSOFGHIFAY-----GADRSEARKQMWI 503
DB 370 -----AYRSPGGAGVRLDGAQLGGEITAHFDSMLVYKMTCRSDPETAVARAQR 418

QY 504 SLKELSIKRGDFTTBYLKLTDFAFENSKITTTGWL-----DGLIQDLRTAERPPAD 556
DB 419 ALAEFTVSG-VATNIGFLRALLREEDFTSKRIATGFIADHPHLLQ-----APPAD 467

RESULT 18
US-10-793-626-218
; Sequence 218, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 218
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-218

Query Match 17.6%; Score 512.5; DB 6; Length 341;
Best Local Similarity 31.7%; Pred. No. 4.5e-33;
Matches 144; Conservative 95; Mismatches 184; Indels 97; Gaps 12

QY 40 KVLICNNGIAAWEIRSIKWAYETTF-----GDERAIEFTVMATPEDLKNVADYIRMDQ 94
DB 4 RCLIANRGEIAVRIIRACRELNIETVAIYAKGDE-----NSLHVSADQ 47

QY 95 YVEVPGGSNNNNYANVDLIVDAERAGVHVAWGWHASENPRIPESLAASKHKIIFIGP 154
DB 48 AICIGEANPLDSYILNIDRIISAANKVTESNVHPGFLSESTNFAK--AVEDNHHIHFIGP 105

QY 155 PGSAMRSLGDKISSTIVAHQADVPCMPWSGTGKETMMSDQGLTVSDDDVYQQACIHTAE 214
DB 106 SKTTMEMMGDKITARTQVTKQAGVPVPGSNDVAQ-----SVD 142

QY 215 EGLEKAEKIGYPMIKASGGGGKIGIRKCTNGBEFKOLYNALVGE-----VPGSPVFMVKL 270
DB 143 ETKLLSKIGTFVVLKAAASGGGGKIGIRVTKGASHLDQALKEAKSSEKGYFNDRRVYVEAF 202

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-858-730-208

Matches 121; Conservative 61; Mismatches 121; Indels 79; Gaps
QY 175 ADVPCMPWSGTGKETMMSDQGLTVSDDDVYQQACIHTAEGLKAEKIGYPMIKASEG 234
DB 14 ANVPVPGS-----EGLIQSDDAKKIAGKIGYPMIIRKATAG 50

QY 235 GGGKIRKCTNGBEFKOLYNALVGEVP-----GSPFVFMKLAGQARHLEVQLLADQYGNAI 290
DB 51 GGGKIRVARDEKELETGYRMTQQEAEATAFNGGLYLEKPIENFRHIEIQIIGDTYGNVI 110

QY 291 SIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEKAVALKLIVGVSAGTVEWLYSPSE 350
DB 111 HLEGRDCTIORRQKLVVEEAPVLSDEKQEMGNAAIRAAKAVNYENAGTIEFIYDLDD 170

QY 351 GSEFAFLNRLQVEHPHTTMSVGNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVI 410
DB 171 NQYFHEMNTRIQVEHPVTMTGVDLVKLQKVANG-----EAL 210

QY 411 DDFSSPESKTORKPOQGHVACRITAENPDTPGKPGMGALTENLFRSSTWGSYFVS 470
DB 211 PF-----KQEDISINGHAIEFRINAENPYKNFMPSPGKITQ-----YLAP 250

QY 471 G-----TSGALHEYADSOFGHIFAYGADRSEARKQMWISLKELSIKRGDFTTVE 519
DB 251 GGFVRIESACYNTYPTPYDSMWAKLIVHEPTREESIMTGIRALSEYVLG-IDTTIP 309

QY 520 YLIKLETTDAFENSKITTTGWL 541
DB 310 FHURLLNHIFRSGEFTKFE 331

RESULT 19
US-10-793-626-804
; Sequence 804, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 804
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-804

Query Match 17.5%; Score 508.5; DB 6; Length 453;
Best Local Similarity 27.7%; Pred. No. 1.4e-32;
Matches 144; Conservative 95; Mismatches 184; Indels 97; Gaps 12

QY 40 KVLICNNGIAAWEIRSIKWAYETTF-----GDERAIEFTVMATPEDLKNVADYIRMDQ 94
DB 4 RCLIANRGEIAVRIIRACRELNIETVAIYAKGDE-----NSLHVSADQ 47

QY 95 YVEVPGGSNNNNYANVDLIVDAERAGVHVAWGWHASENPRIPESLAASKHKIIFIGP 154
DB 48 AICIGEANPLDSYILNIDRIISAANKVTESNVHPGFLSESTNFAK--AVEDNHHIHFIGP 105

QY 155 PGSAMRSLGDKISSTIVAHQADVPCMPWSGTGKETMMSDQGLTVSDDDVYQQACIHTAE 214
DB 106 SKTTMEMMGDKITARTQVTKQAGVPVPGSNDVAQ-----SVD 142

QY 215 EGLEKAEKIGYPMIKASGGGGKIGIRKCTNGBEFKOLYNALVGE-----VPGSPVFMVKL 270
DB 143 ETKLLSKIGTFVVLKAAASGGGGKIGIRVTKGASHLDQALKEAKSSEKGYFNDRRVYVEAF 202

```


US-11-055-822-368
; Sequence 368, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 368
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-368

Query Match 5.7%; Score 167; DB 7; Length 1113;
Best Local Similarity 22.2%; Pred. No. 3.8e-05;
Matches 92; Conservative 69; Mismatches 175; Indels 78; Gaps 18;
QY 149 IIFGPPGSAKSLGDKISSTIVAHQADVPCMPWSGTGKTKTNGEFGKQLYNAVLEVPVS 206
DB 655 IVOLG--GOTPLGLADRL-----KKAGVPVIGTSPAL--DMAEDRGEFGALLNREQLP 704
QY 207 QACIHTA---EEGLEKAEKIGYPMIKASEGGGKIRKCTNGEFGKQLYNAVLEVPVS 263
DB 705 APAGTATSFEEARTVADEISYPLVRPSYVLGRGMEIVYVDEASLEDIYNRATLSSDH 764
QY 264 PVFVKLAGQARHLEVOLLADQVGNALISIFGRDCSVORRHOKIIEEA-----P 311
DB 765 PVLVDRFLDNLAEIDVDALCD--GDEVYLAG-----VMEHIEEAGIHSGDSACALPP 814
QY 312 VTIAPEADARESMEKAAVRLAKLVGVYVAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEM 371
DB 815 MTLGAQDI-EKVREATKKLALGIGV--QGLMNVQYALKDDILYVIANPRASRTVPFVSK 871
QY 372 VSGVNIPIAAQLOVANGIPLYSTRDITLYGMDPRGNEVIDFSPESFEKTKRKP----- 426
DB 872 ATGVNLAKAASRIAVGATIKDLQD----EGMTPEYDGGSLPLDAPIAVKEAVLPFNRFR 927
QY 427 QPOGHVACRIITAEINPDTPGKPGMGALTELNFRSSTSTWGYSVGTSGALHEYADSQFGH 486
DB 928 RPDGKTLDTLSPENKSTGEVWMLAN-----NFGAA---YAKAEAGAFAL-----PTEGT 975
QY 487 IFAYGADREARKQWISLKELSIRGDFRTTVEYLIKLETDAPESNKITGWL 540
DB 976 VFTVYANRD--KRTLILPIQLALNG-----YKILATEG-----TAGML 1012

RESULT 25
US-11-055-822-1000
; Sequence 1000, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1000
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1000

Query Match 5.7%; Score 167; DB 7; Length 1113;
Best Local Similarity 22.2%; Pred. No. 3.8e-05;
Matches 92; Conservative 69; Mismatches 175; Indels 78; Gaps 18;
QY 149 IIFGPPGSAKSLGDKISSTIVAHQADVPCMPWSGTGKTKTNGEFGKQLYNAVLEVPVS 206
DB 655 IVOLG--GOTPLGLADRL-----KKAGVPVIGTSPAL--DMAEDRGEFGALLNREQLP 704
QY 207 QACIHTA---EEGLEKAEKIGYPMIKASEGGGKIRKCTNGEFGKQLYNAVLEVPVS 263
DB 705 APAGTATSFEEARTVADEISYPLVRPSYVLGRGMEIVYVDEASLEDIYNRATLSSDH 764
QY 264 PVFVKLAGQARHLEVOLLADQVGNALISIFGRDCSVORRHOKIIEEA-----P 311
DB 765 PVLVDRFLDNLAEIDVDALCD--GDEVYLAG-----VMEHIEEAGIHSGDSACALPP 814
QY 312 VTIAPEADARESMEKAAVRLAKLVGVYVAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEM 371
DB 815 MTLGAQDI-EKVREATKKLALGIGV--QGLMNVQYALKDDILYVIANPRASRTVPFVSK 871
QY 372 VSGVNIPIAAQLOVANGIPLYSTRDITLYGMDPRGNEVIDFSPESFEKTKRKP----- 426
DB 872 ATGVNLAKAASRIAVGATIKDLQD----EGMTPEYDGGSLPLDAPIAVKEAVLPFNRFR 927
QY 427 QPOGHVACRIITAEINPDTPGKPGMGALTELNFRSSTSTWGYSVGTSGALHEYADSQFGH 486
DB 928 RPDGKTLDTLSPENKSTGEVWMLAN-----NFGAA---YAKAEAGAFAL-----PTEGT 975

QY 497 IFAYGADSEARKOMVSKLSIRGDFRTTVEYLKLELTDAPESNKITIGWL 540
Db 976 VFTVVRND--KRTILPQRLALWG-----YKILATEG-----TAGML 1012

RESULT 26

US-11-055-822-910
; Sequence 910, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 910
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-910.

Query Match 3.8%; Score 110; DB 7; Length 408;
Best Local Similarity 21.6%; Pred. No. 0.27; Indels 88; Gaps 21;
Matches 90; Conservative 66; Mismatches 172;
QY 39 TKVLICNNGIAAVKEIRSKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEV 98
Db 16 TKVLLGSG-----ELGKEVAIAFORLG---LEVHA-----VDRYHA 50
QY 99 PGCSNNNYANVLIVDAERAGHVAWAGHASENPR----LPESLAASKHIFIGP 154
Db 51 PA-----HOVAHFSYVIDMTDAAQVREL-----VERVRPDFVPIETEAATDELVKIEE 99
QY 155 PGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTVSDVYQACIHTAE 214
Db 100 EGLA-----TIVPT-ARAKLTMRGIRKLAEEGLGFTSN-----YEFCL-STFE 143
QY 215 EGLEKAEKIGYPMIKASGGGKGIRKCTNGBEFKQLYNAVL--GEVPGSPVFV---MK 269
Db 144 EFSAAAEKLGYPNVKVPVMSGKQSVLRSDDLQAAWDYANGARVANSRVIVEAFYE 203
QY 270 LAQQAHLVQLLADQYGNNAISIFGRDCSVQRHQKIIEE-APVTIAPEDAREMEKAAV 328
Db 204 FDYEITLLTVRSIDPTTSKPTATWFCPEIGHRQEDGDYVESWQPMWTPR-ALENARSVAA 262
QY 329 RLAKLVGYVSAGTVEMLYSPESGEFAPLELNPLOVEHPT-----TEMVSGVNIIPA-AQ 381

Db 263 RITNALGGRGVGVGVELFVSGD--DVYFSEVSPR---PHDTGLVTLATQRFSEFELHAKAI 317
QY 382 LQVAMGIPLYSIRDITRLY-GMDPRGNE-----VIDFD---FSSPSESFKTOR 424
Db 318 LGLPVDVTLISPGASAVIYGGIESEGYSTGLABALAVAETDLRIFAKPEAFTKRR 373

RESULT 27

US-10-793-626-3294
; Sequence 3294, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3294
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3294

Query Match 3.5%; Score 101.5; DB 6; Length 371;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 34; Conservative 21; Mismatches 62; Indels 21; Gaps 3;
QY 149 IIFIGPPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGKETMMSDQGLTVSDVYQQA 208
Db 119 IPVGVNGVLAASSMDKLVNKQLFHRGLPQLPYI-----SFLRSEYKRYENN 166
QY 209 CIHTABEGLEKAEKIGYPMIKASGGGKGIRKCTNGBEFKQLYNAVLGEVPGSPVFVM 268
Db 167 IIKLVN-----DKLYPVFVKRPNALGSSVGISKCNNEBELK---SGIAEAFQFDRLVI 217
QY 269 KLAGQAHLVQLLADQY 286
Db 218 EGINAREIEVAVLGNDY 235

RESULT 28

US-10-453-372-1010
; Sequence 1010, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263

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; LENGTH: 1579
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-9

Query Match          3.4%; Score 98.5; DB 7; Length 1579;
Best Local Similarity 19.6%; Pred. No. 15;
Matches 125; Conservative 68; Mismatches 198; Indels 247; Gaps 27;

QY 4 DHKAVSQFTGGNPLETAPASPVADPIRKQGHSHVIT-----KVLI-----CNNGIAAVKE 53
Db 965 DNKTF-----LSVLPDESSAKVISITGAETITVGENITLRIILVQDAFNVIAGQV 1017
QY 54 IRSIRKWAYETRGDERAIEFTVMAITPDELKVNADYIRMADQYVEVPGGSSNNNYANVDLI 113
Db 1018 RLSAQFTTNITIGD-----TAYTDNNGYAYVNL 1046
QY 114 VDVABERAGYHAYWAGHGHASENPLRPESLAASKHKHIIFFIPGGSAMRSLGDKISSTIVAQ 173
Db 1047 ---STQPGYVYVATLDDNNSS-KVDVNVANGKLELTSSKPEITVHNSEG--ITLTATAR 1100
QY 174 HADVCEP-----WSGTGIKETWMSDQGLTVSDD---VYQQAACI-----210
Db 1101 NARGELMPGQIITFSVTPPEGATLSNTGEVLTDQSGQAKVTLTSDKVNVTVTVAIMGKQVP 1160
QY 211 -----HTAE-----EGLEKA-----EKIGYPM-IKASEGGG 236
Db 1161 VQSQVTVAVKADAKTAHVVSVVASPDITADGIDSDTITSRVEDDYGFPEGVVDISHGLD 1220
QY 237 GKG-----IRKCTNGEFPQLYN-----AVLGEVPG-----262
Db 1221 TKGSPVNIPTTRTDQSGQVTAITSTLAEITLVNVQVEGTANQSATITLVAGTADSKS 1280
QY 263 ---SPVYMKLAGOARHLEVLQADQYNAISIFGRDCSVORRHQKIIIEAPVTIAPEDA 319
Db 1281 ILSVDVTLKADYQOSAKLTLQDKYGNPI-----VTSDHLEFVQSGPF-----1325
QY 320 RESMEKAAVRLAKL--VGYSAGTVEMWLYSPESGEGFAFLELNPRLOVEHPTTBMVSGVNI 377
Db 1326 -----VNFLKSLDIDYSQRNYGEYTVTVTGKEGTATLIP-----MLNGVH-1366
QY 378 PAAQLQVANGIPLYSTRDITLYGMDPRGNEVIDPDFSSPEFQKQKPOQGHVVACR-436
Db 1367 -----QANLSISLNGIQSIKEM-----SGHVTANNH 1392
QY 437 ---ITAENPDPTGFKPGMGALTELNFRSS-----TSTWGYFSVGTSGALHEYADSQFGH 486
Db 1393 TSTAKFPFSEGAGAYTTLNNDNFAGKTGVDYDMFSSQGWVSDASGKVS-----1443
QY 487 IFYAGADRSEARKQWVISLKELSIKELSGRDFRTTVEYLKL 524
Db 1444 -FANIGD-----QTSVTISAVPROGG--TTYQTLLKL 1472

RESULT 30
US-11-143-980-50
; Sequence 50, Application US/11143980
; Publication NO. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complete
; TITLE OF INVENTION: Polyketide
; FILE REFERENCE: AM-1014260S
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483

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; APPLICANT: University of Sheffield
; APPLICANT: Biosynthesis Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629MO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-316

Query Match          3.3%; Score 96; DB 6; Length 393;
Best Local Similarity 22.6%; Pred. No. 3.2;
Matches 42; Conservative 25; Mismatches 71; Indels 48; Gaps 7;

Qy 130 CHASE-NRPLPESLAASKHIF---IGPPG-----SAMSRLG 163
Dy 107 GEALISQLKSSGGQYDAVFPLLHGPNGEDGTIOGLEVLDPVYVNGVLSAASSM- 165
Qy 164 DKISSTIVAQHADVPCMPWSGTGKETWMSDQGLTVSDVVQQAICHTABEGLEKAEKI 223
Dy 166 DKLVMKQLFEHRLGPQLYI-----SFLSEYKVEYHNILKLVN-----DKL 207
Qy 224 GYPVMIKASEGGGKIRKCTNGEEFKQLYNALGEVPGSPVFMKLAGQARHLEVLQ 283
Dy 208 NYPVFKPANLSSVIGSKCNNEALKE---GIKEAFQDRKLVEIQGVNAREIEVAVLG 264
Qy 284 DOYGNA 289
Dy 265 NDYPEA 270

RESULT 34
US-10-519-531-4
; Sequence 4, Application US/10519531
; Publication No. US20050244429A1
; GENERAL INFORMATION:
; APPLICANT: Folks, Thomas M.
; TITLE OF INVENTION: LIVE REPLICATING SPUMAVIRUS VECTOR
; FILE REFERENCE: 14114.0373U2
; CURRENT APPLICATION NUMBER: US/10/519,531
; PRIOR APPLICATION NUMBER: PCT/US03/20325
; PRIOR FILING DATE: 2004-12-27
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,630
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-519-531-4

Query Match          3.3%; Score 96; DB 6; Length 512;
Best Local Similarity 19.3%; Pred. No. 4.7;
Matches 88; Conservative 55; Mismatches 179; Indels 134; Gaps 18;

Qy 14 GNPLETAPSPVADPIRKGQGHSHVTKVLCNNGIAAVKEIRSIRKWA-----YETFGDER 69
Dy 123 GHSSQVSNYPVQNIQGMVHQAISP-----RTLNWVKVVEEKAFSEV 168
Qy 70 AIBFTVM---ATPEDLKNADYIRMDAQYVEVPGGSGNNNYANVDLI-----VDVAERAG 121
Dy 169 IPMFSALSEGATPQDLNMLNTV-----GG-----HQAAMQMLKETINEEAAEWDR 214
Qy 122 VHAWWAG-----WGHASENRLPES-----LAASKHKII 150
Dy 215 VHPVHAGPIAPGQWRPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIV 274
Qy 151 FIGPPGSAM-----RSLGDKISSTIVAQHADVPCMPWSGTGKETWMSDQGLTV 200
Dy 275 RMYSPTSILDIRQGPKEPRDYVDRFYKTLRAEQASQEVKNW---MTEILLVQNANPDC 330
Qy 201 SDDVYQOACHTABEGLEKAEKIGYPVMIKASEGGGKIRKCTNGEEFKQLYNALGEV 260
Dy 331 KTIKALGPAATLEE-----MMTACQGVGGPGHKARVLAEAMSQVNTSAT--- 375
Qy 261 PGSPVFMKLAGQARHLEVLQADQYGNALISIFGRDCSVORR-----HOKIIEEA 310
Dy 376 -----IMMORGNFRNORKIVKFCNGKEGHI-ARNCRAPRKKGCWCKGEGHO----- 422
Qy 311 PVTIAPEDARESMKAAVRLAKLVGVYAGTVEWLYS-PESGGEFAFLELNPRLQVEHPTT 369
Dy 423 -----MKDCTEROANFLGKIWPSYKGRPGNFLQSRPEPTAPPFLQSRPE-PTAPPEE 473
Qy 370 EMVSGVNIPA-AQLQVAMGPIYSIRDITLYGMDP 404
Dy 474 SPRSGVETTTTPSQKQEPIDKELYPLTSLRSLFGNDP 509

RESULT 35
US-10-519-531-5
; Sequence 5, Application US/10519531
; Publication No. US20050244429A1
; GENERAL INFORMATION:
; APPLICANT: Folks, Thomas M.
; TITLE OF INVENTION: LIVE REPLICATING SPUMAVIRUS VECTOR
; FILE REFERENCE: 14114.0373U2
; CURRENT APPLICATION NUMBER: US/10/519,531
; CURRENT FILING DATE: 2004-12-27
; PRIOR APPLICATION NUMBER: PCT/US03/20325
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,630
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-519-531-5

Query Match          3.3%; Score 96; DB 6; Length 512;
Best Local Similarity 19.3%; Pred. No. 4.7;
Matches 88; Conservative 55; Mismatches 179; Indels 134; Gaps 18;

Qy 14 GNPLETAPSPVADPIRKGQGHSHVTKVLCNNGIAAVKEIRSIRKWA-----YETFGDER 69
Dy 123 GHSSQVSNYPVQNIQGMVHQAISP-----RTLNWVKVVEEKAFSEV 168
Qy 70 AIBFTVM---ATPEDLKNADYIRMDAQYVEVPGGSGNNNYANVDLI-----VDVAERAG 121
Dy 169 IPMFSALSEGATPQDLNMLNTV-----GG-----HQAAMQMLKETINEEAAEWDR 214
Qy 122 VHAWWAG-----WGHASENRLPES-----LAASKHKII 150
Dy 215 VHPVHAGPIAPGQWRPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIV 274
Qy 151 FIGPPGSAM-----RSLGDKISSTIVAQHADVPCMPWSGTGKETWMSDQGLTV 200
```

Db 275 RMYSPSILDIRQGPKEPRDYDRFYKTLRAEQASQEVKNW-----MTETLLVQNANPDC 330
Qy 201 SDDVYQACIHTAEGLKAEKIGYPMIKASEGGGGKIRKCTNGEBFKQLYNVAVLGEV 260
Db 331 KTIILKALGPAATLBE-----NMTACQGVGGFGHKARVLAEAMSQVTSAT--- 375
Qy 261 PGSPVFMVFKLAGQARHLEVLQADQYGNASIFGRDCSVQRR-----HOKIITEEA 310
Db 376 -----IMMORGNFRNQRKIYKFCNCGKEGHI-ARNCEAPRKCGKCKGKEHQ----- 422
Qy 311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMLYS--PESGEFAFLELNPRLOVEHPTT 369
Db 423 -----MKDCTERQANFLKINPSYKGRPCGNFLOSRRPEPTAPPFLQSRDE-PTAPPEE 473
Qy 370 EMVSGVNIPA-AOLQVANGIPLYSIRDITLYGMDP 404
Db 474 SFRSGVETTPSQKQEPIDKELYPLTSLRSLFGNDP 509

RESULT 36

US-11-055-822-1146
; Sequence 1146, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1146
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

US-11-055-822-1146

Query Match 3.3%; Score 96; DB 7; Length 610;
Best Local Similarity 20.9%; Pred. No. 6;
Matches 102; Conservative 59; Mismatches 188; Indels 140; Gaps 22;
Qy 64 TFGDERAIEFTVMATP--EDLKNADYIRMDQYVEVPGGSNNNY----- 107
Db 145 TSEDGTGFEVDVKLPYLRDLGVTAIELLPVQPF-----GGRNWGYDGLVLAHVHAGYGG 200
Qy 108 -ANVDLIVDAERAGVHAVW-----AGW-----GHAS 133
Db 201 PAGLKKLIDASHQAGI-AVYLDVVYVNHFGPDGNYNCGFPTSGSGTGMDVNVNINHDS 259

Qy 134 ENPRLPESLAASKHKIIFIGPPG---SAMRSLGDKISSTIVAQHADVPCMPWSGTG----- 186
Db 260 DEVR-NYILDAARQWFEDFHVGLRLDAVHSLDDRGAYSLLAQLTWVAEDVSAQTGIPRS 318
Qy 187 -IKETWMSDQGFITVSD-----DVYQACIHTAEGLKAEKIGYPMIKASEGGGKG 239
Db 319 LIAESELNDPKFVTSRAGSGFLDAQWDDIHIALHALVSGRMGY-----YSDFGSVD 373
Qy 240 IRKCTNGEEFKQL--YNVAVLGEVPGSPVFMVFKLAGQARHLEVLQADQYGNASIFGRDC 297
Db 374 LAK-TLREVEPHTGNTYGRNHRDPVH-PDITPASRFVYTTTTHDQTGNNR-AIGDRPS 430
Qy 298 SVORRHQKIIEEAPVTIAP-----BDA 319
Db 431 TLTTPGOOVLKAAIYSSPYTPMLFMGEFGATPPFAFFCSHTDPELNRLTSEGRKREFA 490
Qy 320 RESMEKAAVRLAKLVGYVSAGTVEMLYSPESGEF-----AFLELNPRLOVEHP--- 371
Db 491 RLGNADDDIPSPELESTFTSSKLDWEFTAQRINDAYKQLLHRLHTLGFSPQNLTLLEV 550
Qy 372 VSGVNIPAAQLQVAMG---IPLYSIRDITLYGMDPRGNEVIDFDFFSSPESFKTRKPQ 427
Db 551 EHGEN---WLSMANGRGRILANFSDDTIV-----PLGGELI-YSTSPVTVDTSITLQ 600
Qy 428 PQGHVACR 436
Db 601 PNGFAILTR 609

RESULT 37

US-11-124-291-6
; Sequence 6, Application US/11124291
; Publication No. US20050266536A1
; GENERAL INFORMATION:
; APPLICANT: WOLF, ANDREAS
; APPLICANT: SCHISCHKA, NATALIE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: MORBACH, SUSANNE
; APPLICANT: KRAEMER, REINHARD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-AMINO ACIDS USING
; FILE REFERENCE: 223168USOX
; CURRENT APPLICATION NUMBER: US/11/124,291
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/212,219
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/316,276
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: DE 101 39 062.9
; PRIOR FILING DATE: 2001-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-124-291-6

Query Match 3.3%; Score 96; DB 7; Length 610;
Best Local Similarity 20.9%; Pred. No. 6;
Matches 102; Conservative 59; Mismatches 188; Indels 140; Gaps 22;
Qy 64 TFGDERAIEFTVMATP--EDLKNADYIRMDQYVEVPGGSNNNY----- 107
Db 145 TSEDGTGFEVDVKLPYLRDLGVTAIELLPVQPF-----GGRNWGYDGLVLAHVHAGYGG 200
Qy 108 -ANVDLIVDAERAGVHAVW-----AGW-----GHAS 133
Db 201 PAGLKKLIDASHQAGI-AVYLDVVYVNHFGPDGNYNCGFPTSGSGTGMDVNVNINHDS 259
Qy 134 ENPRLPESLAASKHKIIFIGPPG---SAMRSLGDKISSTIVAQHADVPCMPWSGTG----- 186

Db 260 DEVR-NYILDAARQWFEHFDGLRLDAVHSLDRGAYSLLAQLTMAEDVSAQTGIPRS 318
Qy 187 -IKETMSDQGLFTVSD-----DVYQOACHTAEGLKAEKIGYPVMIKASGGGGKG 239
Db 319 LIAESELNDPKFVTSREAGGGLDAQWDDIHHAHALVSGERNY-----YSDFGSDVT 373
Qy 240 IRKCTNGEEFKQL--YNAVLEVPSPVFMKLAGQARHLEVLQADYGNATSIIFGRDC 297
Db 374 LAK-TLREVPFHTGNSTYGRNRHGRPH-PDITPASRFVYTTTHDQTNR-AIGDRPS 430
Qy 298 SVORRHOKIIEEAPVTIAP-----ED 319
Db 431 TLTTEQOVLKAAIYSSPYTTPMLFMGEFGATTPPAFFCSHTDPELNRLTSEGRKEFA 490
Qy 320 RESMEKAAVRLAKLVGVYAGTVEWLYSPESGEF-----AFLEINPRLOVEHP---TTEM 371
Db 491 RLGNWADDIPSPELESTFTSSKLDWEFTAEORRINDAYKQLHLRLHTLGFSPQNLTLLEV 550
Qy 372 VSGVNIIPAAQOVAMG---IPLYSIRDITLYGMDPRGNEVIDDFSSPESFKTQKPQ 427
Db 551 EHGEN---WLSMANGRILANFSDDTITV-----PLGGELI-YSFTSPVTVDTTTLQ 600
Qy 428 PQHWACR 436
Db 601 PWGFAILTR 609

RESULT 38

US-11-166-609-18
; Sequence 18, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166.609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 18
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-166-609-18

Query Match 3.3%; Score 95.5; DB 7; Length 544;
Best Local Similarity 19.7%; Pred. No. 5.6;
Matches 103; Conservative 63; Mismatches 192; Indels 165; Gaps 24;
Qy 15 NPLETAPASPVADPIRKGQGHSHVITKVLICNNGI-----AAYKEI 54
Db 3 SPMEEAAMPVTSFPFVAGIHKLIAIFLVLSWILVHKWSLRNKGPRSPFIICATVEQL 62
Qy 55 RSIRK---WAYETGDERAI-----EFTWATPEDLKYNADQVVEVPGGSN 104
Db 63 KNYRHMDHLVEYLSKORTVTVDMPFTSYTYIADP-----VNVEHV-LKTNFTNPKGEVY 117
Qy 105 NNYANVDLIIVDVAERAGVHAW-----AGWGHASENPRLPESLAASKHKIIFIGPPGSA 158
Db 118 RSYMDVLGDGIFNADG---EHWRRKORTASFEPAKSLNDRDFTVVVFREYLSKLSSLSQA 175
Qy 159 -----NRSGLDKISST-----IVAQHADV-----CMPWSGTGKETM----- 191
Db 176 CKAGRVVDMQELFMRMTLDSICKVGFVEIGTSLPDLSPENSFAQAFDAANIIVTLRFDIP 235

Qy 192 -----MSDQGLFTVSDVYQOACHTAE-----EGLEKAEKIGYPM-----IK 230
Db 236 LMRKKFLHVGSALLEQSMKLYDDFTYSVIRRRKAEILQARASGQEKIKHIDILSRFIE 295
Qy 231 ASBGGGGKGIKCTNGEEF---KOLYNVAVLGEVPGS-----PVFMK 269
Db 296 LGEAGDGE-----GGSGDDKSLRDVNLVFIAGRDITATTLSWFTYAMTHPAVDK 349
Qy 270 LAGQARHLEVQ-----LLADQYNA-----ISIFGRDCSVORRHQKIIIEEAPVT--- 313
Db 350 LRRELAFFEDERAREEGVALADAAAGEASFAARVAQFASLLSYDAVGKLVYLHACVTETLR 409
Qy 314 ---IAPEDARESMEK-----AAVRLAKLVGVY---SAGTVEWLYSPESGEF----- 353
Db 410 LYPVAPQDDPKGIVEDDVLDPGTVKRVAGGMVYVYPSMGRMEYNWNGDDAASFRPERMLSGD 469
Qy 354 --AFLEINPRLOVEHPHTTEMVSGVNI---PAAQOVAMGIPL 390
Db 470 GGAFRNASP-----FKFTAFQAGPRICLKGDSAYLQMKWALAI 507

RESULT 39

US-11-052-554A-8
; Sequence 8, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 8
; LENGTH: 1417
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-8

Query Match 3.3%; Score 95.5; DB 7; Length 1417;
Best Local Similarity 23.5%; Pred. No. 22;
Matches 64; Conservative 23; Mismatches 120; Indels 65; Gaps 11;

Qy 231 ASBGGGGKGIKCTNGEEFQKQLYNVAVLGEVPGSPVFMKLAGO---ARHLEVOLLADQYG 287
Db 731 AEGSTASG---WTNNGDGTWTQAIIITLGTAGLEVMPKLNQNAANAAKVTIVAD--- 784
Qy 288 NAISIFGRDCSVORRHQKIIIEEAPVTIAPEDARESMEKAAVRLAKLVGVYVSAGTV---EWL 345
Db 785 -ALLSNQSKVSVAEHDVKAGESITVLVAKDAHNAISGLASLTGTASEGATVSSW- 842
Qy 346 YSPESGEFAP-----LELNPRLQVEHPPTTEMVSGVNIIPAAQOVAMGIPLYSI 393
Db 843 --TEKNGSVYATLTGGKTGELRVNPLFNGQPAATE-----AAQLTVIAG-EMSSA 891
Qy 394 RDITLYGMDPRGNEVIDDFSSPESFKTQKQPOGHVVACRITAEINPDTGFKPG--- 449
Db 892 NSTLVADNKAPTVKTTELTFTVKDAY-----GNPVTGLKPDAPVF 932
Qy 450 MGALTIELNFRSSTSTWG-----YFSGVTGSA 475
Db 933 SGAASTGSRSPSAGNWKENGNGVYVSTLTIGS 964

RESULT 40

US-11-070-080-16
; Sequence 16, Application US/11070080
; Publication No. US20050287625A1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 18:05:02 ; Search time 203 Seconds
(without alignments)
1209.915 Million cell updates/sec

Title: us-10-633-835-2

Perfect score: 2907

Sequence: 1 PPDHKAVSQFIGGNPLETA.....LDGLIQDLTAERPPADLAV 559

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2874	98.9	559	ADJ47651	Adj47651 U. maydis
2	2222	76.4	2214	ADN10916	Adn10916 Phaffia r
3	2166	74.5	2273	AAR98811	Aar98811 Erysiphe
4	2163	74.4	591	ADJ47653	Adj47653 M. grisea
5	2139	73.6	2301	ADN21045	Adn21045 Bacterial
6	2079	71.5	2241	ADN19477	Adn19477 Bacterial
7	2061.5	70.9	2270	AAJ24150	Aaj24150 Candida a
8	2060	70.9	580	ADJ47654	Adj47654 S. cerevi
9	2060	70.9	2000	ABR52730	AbR52730 Protein s
10	2060	70.9	2000	ADK61968	Adk61968 Disease t
11	2060	70.9	2233	ADQ90738	Adq90738 Yeast ace
12	2060	70.9	2233	ADN19345	Adn19345 Bacterial
13	1889.5	65.0	983	ADN19252	Adn19252 Bacterial
14	1889.5	65.0	2000	ADK63986	Adk63986 Disease t
15	1790	61.6	632	ADJ47655	Adj47655 Human ACC
16	1787	61.5	2346	ADQ90744	Adq90744 Human aci
17	1781	61.3	2346	ABP70270	Abp70270 Human aci
18	1781	61.3	2346	ABP59197	Abp59197 Human ace
19	1781	61.3	2346	ABP59195	Abp59195 Human ace
20	1781	61.3	2346	ABP59198	Abp59198 Human ace
21	1780	61.2	2348	ABP59490	Abp59490 Drosophil
22	1780	61.2	2348	AAO19075	Aao19075 Drosophil
23	1780	61.2	2348	ABP33866	Abp33866 Drosophil
24	1775	61.1	2288	AAH86033	Aah86033 Bovine ac

25	1774	61.0	2324	2	AAR05707	Aar05707 Acetyl-Co
26	1769.5	60.9	2420	8	ABM83569	Abm83569 Human dia
27	1769.5	60.9	2458	6	ABP59211	Abp59211 Human str
28	1769.5	60.9	2487	6	ABM84649	Abm84649 Human SEC
29	1769.5	60.9	2498	5	ABU65149	Abu65149 Human NOV
30	1769.5	60.4	2498	8	ADN61949	Adn61949 Human nov
31	1738	59.8	774	8	ADJ47656	Adj47656 Human ACC
32	1697.5	58.4	2206	8	ADN03634	Adn03634 Antipsoi
33	1669.5	57.4	2483	8	ADQ90746	Adq90746 Human ace
34	1669.5	57.4	2483	8	ADQ39507	Adq39507 Human myo
35	1669.5	57.4	2483	9	AEA33628	Aea33628 Human ACC
36	1604	55.2	555	8	ADJ47652	Adj47652 P. infest
37	1591.5	54.7	1096	8	ADQ39504	Adq39504 Human myo
38	1591.5	54.7	2486	4	AAU32848	Aau32848 Novel hum
39	1583	54.5	2240	2	AAR67819	Aar67819 Acetyl Co
40	1581.5	54.4	2359	5	ABB91251	Abb91251 Herbicida
41	1579	54.3	2204	3	AAG50615	Aag50615 Arabidops
42	1579	54.3	2243	8	ADN72177	Adn72177 Thale cre
43	1579	54.3	2254	2	AAR76949	Aar76949 ACCase. 2
44	1578	54.3	2254	2	AAJ22129	Aaj22129 Arabidops
45	1578	54.3	2254	2	AAJ40598	Aaj40598 Arabidops

ALIGNMENTS

RESULT 1
ADJ47651.
ID ADJ47651 standard; protein; 559 AA.
AC ADJ47651;
XX
DT 06-MAY-2004 (first entry)
XX
DE U. maydis ACCase BC domain SEQ ID NO:2.
XX
KW ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
KW biotin carboxylase domain; BC domain; fungicide.
XX
OS Ustilago maydis.
XX
PN WO2004013159-A2.
XX
PD 12-FEB-2004.
XX
PF 04-AUG-2003; 2003WO-US024356.
XX
PR 05-AUG-2002; 2002US-0401170P.
XX
PA (CROP-) CROPSOLUTION INC.
XX
PI Ellich TD, Volrath SL, Weatherly SC;
XX
DR WPI; 2004-180421/17.
XX
PT Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
PT biotin binding domain and carboxy transferase domain, and having
PT functional biotin carboxylase domain, useful for identifying ACCase
PT inhibitors/activators.
XX
PS Claim 8; SEQ ID NO 2; 56pp; English.
XX
CC The invention relates to a novel peptide (I) comprising an acetyl CoA
CC carboxylase (ACCase) having a deleted biotin binding domain, having a
CC deleted carboxy transferase domain, and having a functional biotin
CC carboxylase domain. A peptide of the invention is useful for identifying
CC acetyl CoA carboxylase inhibitors or activators, which involves combining
CC the peptide and a compound to be tested for the ability to bind to the
CC biotin carboxylase domain, under conditions that permit binding to the
CC biotin carboxylase domain, determining whether or not the compound binds
CC to the biotin carboxylase domain, the presence of binding indicating the
CC compound is or may be an Acetyl CoA carboxylase inhibitor or activator.
CC The method further involves employing the identified binding compound in

an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence represents an Accase BC domain of the invention.

XX Sequence 559 AA;

Query Match 98.9%; Score 2874; DB 8; Length 559;

Best Local Similarity 98.9%; Pred. No. 5.2e-261;

Matches 553; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 PPDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVEIRSKW 60

DB 1 PPDHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVEIRSKW 60

QY 61 AYETFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGSNNNYANDLIVDAERA 120

DB 61 AYETFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGSNNNYANDLIVDAERA 120

QY 121 GVHAWAGWGHASNPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180

DB 121 GVHAWAGWGHASNPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180

QY 181 PWSGTGKETWMSDQGLTWSDDVYQACIHTAEGLKAEKIGYPWMIKASGGGKGI 240

DB 181 PWSGTGKETWMSDQGLTWSDDVYQACIHTAEGLKAEKIGYPWMIKASGGGKGI 240

QY 241 RKTNGEFPKQLYNAVLEVPVGVFVWKLQAGARHLEVQLLADQYGNALISIFGRDCSVQ 300

DB 241 RKTNGEFPKQLYNAVLEVPVGVFVWKLQAGARHLEVQLLADQYGNALISIFGRDCSVQ 300

QY 301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEFAFLNLP 360

DB 301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEFAFLNLP 360

QY 361 RLOVEHPTTEMVSGVNIPTAQLOVAMGIPIYSIRDIRTLVGMGRGNEVIDFDFSSPESF 420

DB 361 RLOVEHPTTEMVSGVNIPTAQLOVAMGIPIYSIRDIRTLVGMGRGNEVIDFDFSSPESF 420

QY 421 KTORKPOQGHVACRITAEENPDGFKPGKALTELNFIRSTSTWGYFSYGTSGALHEYA 480

DB 421 KTORKPOQGHVACRITAEENPDGFKPGKALTELNFIRSTSTWGYFSYGTSGALHEYA 480

QY 481 DSQFGHIFAYCADRSEARKQWISLKELISIRGDFRTTVEYLKLETDAPESNKITGWL 540

DB 481 DSQFGHIFAYCADRSEARKQWISLKELISIRGDFRTTVEYLKLETDAPESNKITGWL 540

QY 541 DGLIQDLRLTAERPDLAV 559

DB 541 DGLIQDLRLTAERPDLAV 559

RESULT 2

ADN10916

ID ADN10916 standard; protein; 2214 AA.

XX

AC ADN10916;

XX

DT 01-JUL-2004 (first entry)

XX

DE Phaffia rhodozyma acetyl-CoA carboxylase.

XX

KW Acetyl-CoA carboxylase; enzyme; astaxanthin; pigment; antioxidant.

XX

OS Xanthophyllomyces dendrorhous.

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WO2004029232-A2.

08-APR-2004.

25-SEP-2003; 2003WQ-EP010683.

27-SEP-2002; 2002EP-00021625.

(STAM) DSM IP ASSETS BV.

Hoshino T, Ojima K, Setoguchi Y;

WPI; 2004-329883/30.

N-PSDB; ADN10914, ADN10915.

New acetyl-CoA carboxylase polynucleotide derived from Phaffia rhodozyma or Xanthophyllomyces dendrorhous, useful for producing a recombinant vector or for increasing microbial production of carotenoids.

Claim 1; SEQ ID NO 3; 82pp; English.

The present sequence is the protein sequence of the acetyl-CoA carboxylase (ACC) gene of Phaffia rhodozyma (ATCC 74438). The sequence shows 56.28% amino acid sequence identity to a known ACC from *Emicella nidulans*. ACC is an enzyme involved in fatty acid biosynthesis. Its substrate is acetyl-CoA, which is also involved in the carotenogenic pathway of *P. rhodozyma*. A claimed method for producing ACC comprises culturing a recombinant organism containing a vector comprising an ACC polynucleotide. Also claimed is a recombinant organism in which gene expression of ACC is reduced as a result of antisense technology, site-directed mutagenesis, error-prone PCR or chemical mutagenesis. The recombinant organism is preferably *P. rhodozyma* or *Xanthophyllomyces dendrorhous* containing a vector comprising an antisense polynucleotide. It is used in a claimed process for producing carotenoids such as astaxanthin, beta-carotene, lycopene, zeaxanthin and canthaxanthin. The method is useful for increasing microbial production of carotenoids such as astaxanthin, which has antioxidant properties and is used as a colouring agent especially of farmed fish.

Sequence 2214 AA;

Query Match 76.4%; Score 2222; DB 8; Length 2214;

Best Local Similarity 76.3%; Pred. No. 1.4e-198;

Matches 424; Conservative 49; Mismatches 83; Indels 0; Gaps 0;

QY 4 DHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVEIRSKWYE 63

DB 4 DHKAVSQFIGNPLETAPASPVADFIKQGHSHVITKVLICNNGIAAIVEIRSKWYE 63

QY 64 TFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGSNNNYANDLIVDAERAAGVH 123

DB 64 TFGDERALEFTVMATPEDLKNADYIRMDQYVEVPGSNNNYANDLIVDAERAAGVH 123

QY 124 AWAGWGHASNPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMWS 183

DB 124 AWAGWGHASNPRLPSLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMWS 183

QY 184 GTGKETWMSDQGLTWSDDVYQACIHTAEGLKAEKIGYPWMIKASGGGKGIKRC 243

DB 184 GTGKETWMSDQGLTWSDDVYQACIHTAEGLKAEKIGYPWMIKASGGGKGIKRC 243

QY 244 TNGEFPKQLYNAVLEVPVGVFVWKLQAGARHLEVQLLADQYGNALISIFGRDCSVQRH 303

DB 244 TNGEFPKQLYNAVLEVPVGVFVWKLQAGARHLEVQLLADQYGNALISIFGRDCSVQRH 303

QY 304 OKIIEEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEFAFLNLP 363

DB 304 OKIIEEAPVTIAPEDARESMKAAVRLAKLVGVYSAGTVWLYSPESGEFAFLNLP 363

QY 364 VEHPTEMVSGVNIPTAQLOVAMGIPIYSIRDIRTLVGMGRGNEVIDFDFSSPESK 423

DB 364 VEHPTEMVSGVNIPTAQLOVAMGIPIYSIRDIRTLVGMGRGNEVIDFDFSSPESK 423

QY 424 RKPOQGHVACRIATAENPDGFKPCMGALTELNFRSSTSTWGYSVTSGLALHEYADSQ 483
 DB 424 RKPRPKGHVACRIATSENPDEGFKPSAGDIQELNFRSNTNMGYSFVGATGGIHSFADSQ 483
 QY 484 FGHIFAYGADRSEARKOMVISLSELSIRGDFRTTVEYLILKLETDAPESNKITTTGWLDDGL 543
 DB 484 FGHVFAVGSDDTARKKNVIALKELLSIRGDFRTTVEYLILKLETSDFEQNALTTAWLDDGL 543
 QY 544 IQDLRTAERPPADLAV 559
 DB 544 ITNKLTSERPPDSLAV 559

RESULT 3

AAR98811 standard; protein; 2273 AA.

XX AC AAR98811;
 DT 16-OCT-2003 (revised)
 DT 10-FEB-1997 (first entry)
 XX Erysiphe graminis acetyl coenzyme A carboxylase.
 XX Acetyl coenzyme A carboxylase; ACoCase; powdery mildew; fungus; ACCase;
 KW fatty acid biosynthesis; EC 6.4.1.2.
 XX Blumeria graminis; f.sp.hordei.
 XX FR2727129-A1.
 XX 24-MAY-1996.
 XX 21-NOV-1994; 94FR-000141187.
 XX 21-NOV-1994; 94FR-000141187.
 XX (RHON) RHONE POULENC AGROCHIMIE.
 XX Lebrun M, Grosjean CMC, Hollomon DW;
 PI WPI; 1996-270416/28.
 DR N-PSDB; AAT30758.

XX Microorganism with specific biochemical activity deleted by mutation -
 PT and complemented, used in system to identify cpds with plant protecting
 PT activity, also new gene for acetyl coenzyme A carboxylase.
 XX Example 2; Page 16-22; 26pp; French.
 CC The present sequence is the deduced amino acid sequence of acetyl
 CC coenzyme A carboxylase (ACoCase, EC.6.4.1.2) from powdery mildew
 CC (Erysiphe graminis f.sp. hordei 23DS). It was deduced from a 8123 bp DNA
 CC sequence isolated from an EcoRI genomic library by screening with a
 CC fragment of the Saccharomyces cerevisiae ACoCase gene. The amino acid
 CC sequence has 63 % identity and 77 % similarity to the yeast enzyme; it
 CC also has 47 % identity (67 % similarity) with the ACoCase proteins from
 CC rat and chicken. ACoCase activity is the preferred target biochemical
 CC activity in a new screening system. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX Sequence 2273 AA;

Query Match 74.5%; Score 2166; DB 2; Length 2273;
 Best Local Similarity 73.3%; Pred. No. 2.7e-193;
 Matches 407; Conservative 61; Mismatches 87; Indels 0; Gaps 0;
 QY 5 HKAVSOFIGNPFIETAPASVAFIRKQGHSHVITKVLICNNGIAAAVKESIRKWAYET 64
 DB 27 HQIAEHFIGNKLNASPSDVKEFVAKDGHGTVITNVLIANNGLAAVKESIRKWAYET 86
 QY 65 FGDERAIEFTVMTPEDLKKNADYIRMAQYVEVPGSGNNNNYANVDLIVDAERAGVHA 124

DB 87 FGDERAIEFTVMTPEDLQANADYIRMAQYVEVPGSGTNNNNCANVELIVDAERMDVHA 146
 QY 125 VWAGWGHASENPRLPESLAASKHKIIFIGPPGAMRSLGDKISTTIVAOHADVPCKMWSG 184
 DB 147 VWAGWGHASENPRLPESLAASKPKIIFIGPPGAMRSLGDKISTTIVAOHAKVPCIPWSG 206
 QY 185 TGKETMMSDQGLTVDYQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCT 244
 DB 207 TGVDOVEVNDGIVTVDEKVMKGVQSQWQGLEKAREIGFPVMIKASEGGGKGIRKVD 266
 QY 245 NGEFFKOLYNALVGEVPGSPVFMKLAGOARHLEVLQADYGNATISIFORDCSVQRHQ 304
 DB 267 SDEGFEALYKAAANEIPGSEIFIMKLAGNARHLEVLQADYGNATISIFORDCSVQRHQ 326
 QY 305 KIIEEAPVTIAPEDAREMEKAARLAKLVGYVSAGTVWLYSPESGEFAFLELNPELOV 364
 DB 327 KIIEEAPVTIATSTTFQMEKAARVLRGLVGYVSAGTVWLYSHAEKDFLELNPELOV 386
 QY 365 EHPTTEMVSGVNIIPAAQLQVAMGIPLYSIRDIRTLTGMDPRGNEVIDDFSSPSFKTOR 424
 DB 387 EHPTTEMVSGVNLPAALQIAMGLPLHRIIRDIRLLYGVDPQGSTSIDDFSKDSSSTQR 446
 QY 425 KPQPOGHVACRIATAENPDGFKPCMGALTELNFRSSTSTWGYSVTSGLALHEYADSQ 484
 DB 447 RPTPKGHTTACRTITSEDPGEFKPSGMMHNLNFRSSSNVWGYPSVGTAGGIHSFSDSQ 506
 QY 485 GHIFAYGADRSEARKOMVISLSELSIRGDFRTTVEYLILKLETDAPESNKITTTGWLDDGL 544
 DB 507 GHIFAYGENRSARKHVMVALKELLSIRGDFRTTVEYLILKLETPAPEDNTITTTGWLDEL 566
 QY 545 QDLRTAERPPADLAV 559
 DB 567 SNKLTAERPPDILAV 581

RESULT 4

ADJ47653
 ID ADJ47653 standard; protein; 591 AA.
 XX ADJ47653;
 XX 06-MAY-2004 (first entry)
 DE M. grisea ACCase BC domain SEQ ID NO:6.
 KW ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
 KW biotin carboxylase domain; BC domain; fungicide; rice blast fungus.
 OS Magnaporthe grisea.
 XX WO2004013159-A2.
 PD 12-FEB-2004.
 PF 04-AUG-2003; 2003WO-US024356.
 PR 05-AUG-2002; 2002US-0401170P.
 XX (CROP-) CROPSOLUTION INC.
 PA Ellich TD, Volrath SL, Weatherly SC;
 PI WPI; 2004-180421/17.
 DR Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
 PT biotin binding domain and carboxy transferase domain, and having
 PT functional biotin carboxylase domain, useful for identifying ACCase
 PT inhibitors/activators.
 XX Claim 9; SEQ ID NO 6; 56pp; English.
 XX The invention relates to a novel peptide (I) comprising an acetyl CoA


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Db      6 HNLAPHFIGNRLNENAPSKVKDFVASHDGHVITNVRFLALPAVQRTFEXHLLVQVLI 65
QY      44 CNGIAAVKEIRSIKWAYETFGDERAIEFTVMAATPEDLKVADYIRMAQYVEVPGSN 103
Db      66 ANNGIAAVKEIRSVKWAYETFGDERAIEFTVMAATPEDLQANADYIRMAHYVEVPGTN 125
QY      104 NNNYANVDLVDVAERAGVHVAWAG-----GHASENPRPESL 142
Db      126 NNNYANVELLVDIAERMDVHVAWAGCVDKSPASGVDMKILTVRIGGHASENPKLPESL 185
QY      143 AASKHKIIFIPGPGSAMRSLGDKISSTIVAQAHDVPCMPMSGTGCIKETWMSDQGFITVSD 202
Db      186 AASPKKIVIFIPGPGSAMRSLGDKISSTIVAQAHDVPCIPMSGTGVSEVKVDNDGIVTVPD 245
QY      203 DVTQQAQCIHTAEGLEKAEKIGYPVMIKASEGGGGKIRKCTNGEBFKQLYNALVGEVPG 262
Db      246 DVTYKGCVSQWEGLEKAREIGFPVMIKASEGGGGKIRKVLNEDNFESLYNAAASEIPG 305
QY      263 SPVFMKLAGQARHLEVQVLLADQYGNALSTFGSDCSVQREHOKIIEAPVTIAPEDARES 322
Db      306 SPIFIMKLADSAARHLEVQVLLADQYGNALSTFGSDCSVQRRHQKIEAPVTIAKPTTFKA 365
QY      323 MEKAAVRLAKLVGVSGAGTVEMLYSPESGFAFLELNPRLOVEHPHTEMVSGVNIAPAAQL 382
Db      366 MEAAVRLGLVGVSGAGTVEMLYSHADKXYFLELNPRLOVEHPHTEMVSGVNLPAQQL 425
QY      383 QVAMGPIYLRIDIRTYLGMNDPRGNEVDPDFSPSPSFKTQRPQGHVACRITAEANP 442
Db      426 QVAMGPIYLRIDIRTYLGMNDPRGNEVDPDFSPSPSFKTQRPQGHVACRITAEANP 485
QY      443 DTGFKPGMGTALTELNRSSSTTWGYSVGTSGALHEVADSOFGHIYAGADRSEARKQMV 502
Db      486 GEGFKPSNGVLHDLNFRSSNWMGYSVGSAGGIHFSQSGFHIYAGENRAASRKHV 545
QY      503 ISLKELSGRDFRTTVEYLKILETDAFESNKITTGWLGLIQLDRLTAEPPADLAV 559
Db      546 VALKELSGRDFRTTVEYLKILETDAFESNTITGWLDELISKLTAEPPADLAV 602.

RESULT 6
ADN19477
ID  ADN19477 standard; protein; 2241 AA.
AC  ADN19477;
DT  02-DEC-2004 (first entry)
DE  Bacterial polypeptide #2130.
KW  Recombinant DNA construct; transformed plant; improved plant property;
KW  cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW  pathogen tolerance; pest tolerance; plant disease resistance;
KW  cell cycle pathway modification; plant growth regulator;
KW  homologous recombination; seed oil yield; protein yield; carbohydrate;
KW  nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW  bacterial polypeptide.
OS  Bacteria.
PN  US2003233675-A1.
XX  18-DEC-2003.
XX  20-FEB-2003; 2003US-00369493.
XX  21-FEB-2002; 2002US-0360039P.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.

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XX  Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI  WPI; 2004-061375/06.
XX  New recombinant DNA construct comprising a promoter positioned to provide
XX  for expression of a polynucleotide encoding a polypeptide from a
XX  microbial source, useful for producing plants with improved properties.
XX  Claim 1; SEQ ID NO 2130; 122pp; English.
XX  The invention relates to a recombinant DNA construct comprising a
XX  promoter functional in a plant cell, where the promoter is positioned to
XX  provide for expression of a polynucleotide encoding a polypeptide from a
XX  microbial source. The invention also relates to a transformed plant
XX  comprising the recombinant DNA construct and a method of producing a
XX  transformed plant having an improved property. The plant is a crop plant
XX  such as maize or soybean. The method of producing a transformed plant
XX  having an improved property comprises transforming a plant with the
XX  recombinant DNA construct and growing the transformed plant, where the
XX  polynucleotide or polypeptide is useful for improving plant properties.
XX  The recombinant DNA construct is useful for producing plants with
XX  improved plant properties, e.g. improved cold, heat or drought tolerance,
XX  tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX  increased resistance to plant disease, better growth rate by modification
XX  of the cell cycle pathway with plant growth regulators, increased rate of
XX  homologous recombination, modified seed oil or protein yield and/or
XX  content, improved yield by modification of carbohydrate, nitrogen or
XX  phosphorus use and/or uptake, by modification of photosynthesis or by
XX  providing improved plant growth and development under at least one stress
XX  condition, improved lignin production or improved galactomannan
XX  production. This sequence represents a bacterial polypeptide used in the
XX  scope of the invention. Note: The sequence data for this patent did not
XX  form part of the printed specification but was obtained in electronic
XX  format from USPTO at seqdata.uspto.gov/sequence.html.
XX  Sequence 2241 AA;

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Query Match 71.5%; Score 2079.5; DB 8; Length 2241;
Best Local Similarity 71.4%; Pred. No. 3.7e-185;
Matches 394; Conservative 62; Mismatches 95; Indels 1; Gaps 1;
QY 9 SQFIGGNPLETAPSPADVADIRKOGSHSVITKVLICNNGIAAIVKEIRSIKWAYETFGDE 68
Db 1 NHILGGSLDKAPAGKVDYIASHGGHTVITSLIANNGIAAIVKEIRSIKWAYETFNNE 60
QY 69 RAIEFTVMAATPEDLKVADYIRMAQYVEVPGSGNNNNYANVDLVDVAERAGVHVAWAG 128
Db 61 RAIKFTVMAATPEDLKVADYIRMAQYVEVPGSGNNNNYANVELLVDIAERNVHVAWAG 120
QY 129 WGHASENPRLPESLAASKHKIIFIPGPGSAMRSLGDKISSTIVAQAHDVPCMPWSGTGK 188
Db 121 WGHASENPKLEMLSASSKIVIFIPGPGSAMRSLGDKISSTIVAQSARVPCMSWSGNELD 180
QY 189 ETWMSDQ-GFLTVDSDVYQQAQCIHTAEGLEKAEKIGYPVMIKASEGGGGKIRKCTNGE 247
Db 181 QVRIDEETNIVTVDDDDVYQKACIRSAEAGIAEAEKIGYPVMIKASEGGGGKIRQVTSFE 240
QY 248 EFKQLYNALVGEVPGSPVFMKLAGQARHLEVQVLLADQYGNALSTFGSDCSVQRRHQKII 307
Db 241 KFAQAFQVLDLPGSPVFMKLAGQARHLEVQVLLADQYGNALSTFGSDCSVQRRHQKII 300
QY 308 EAPVTIAPEDARESMEKAAVRLAKLVGVSGAGTVEMLYSPESGFAFLELNPRLOVEHP 367
Db 301 EAPVTIAPATTFHEMERAAVRLGELVGYASAGTIEYLYTEPENDRFYFLELNPRLOVEHP 360
QY 368 TEMVSGVNIAPAAQLQVAMGPIYLRIDIRTYLGMNDPRGNEVDPDFSPSPSFKTQRPQ 427
Db 361 TEMVSGVNLPAQQLQVAMGPIYLRIDIRTYLGMNDPRGNEVDPDFSPSPSFKTQRPQ 420
QY 428 PQGHVACRITAEANPDTGFKPGMGTALTELNRSSSTTWGYSVGTSGALHEVADSOFGHI 487
Db 421 PGGHVCACRITISDEPGEGFKPSSGMIKDLNFRSSNWMGYSVGTAGTAGIHFADSOFGHI 480

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QY 488 PAYGADRSEARKQWVLSIKELSIKSGDFRTTVEYLKLETDAPFNSKITTGWLDGLIQDR 547
 Db 481 FSPAESSRSRKMVVALKELSIKSGDFRTTVEYLKLETDAPFNSKITTGWLDGLIQDR 547
 QY 548 LTAERPPADLAV 559
 Db 541 VTSARPPKMLAV 552

RESULT 7
 AAY24150
 ID AAY24150 standard; protein; 2270 AA.
 XX
 AC AAY24150;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Candida albicans acetyl CoA carboxylase.
 XX
 KW Candida albicans; acetyl CoA carboxylase; ACCase.
 XX
 OS Candida albicans.
 XX
 PN W099332635-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 21-DEC-1998; 98WO-GB003857.
 XX
 PR 20-DEC-1997; 97GB-00026897.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Schnell NF, Dixon GK, Chavda S, Thain JL, Vincent JP;
 XX
 DR WPI; 1999-418931/35.
 DR N-PSDB; AAX88525.
 XX
 XX A polynucleotide encoding an Acetyl-CoA carboxylase gene from Candida
 PT albicans overexpressed in Saccharomyces cerevisiae for purification and
 PT isolation.
 XX
 PS Claim 7; Fig 5; 40pp; English.
 XX
 CC The present sequence represents acetyl CoA carboxylase (ACCase) isolated
 CC from Candida albicans. The C. albicans ACCase is used in an assay to
 CC identify inhibitors of the enzyme. This is useful in pharmaceutical
 CC research. Inhibitors of ACCases are useful as antifungal agents. The
 CC invention also provides a novel expression system using Saccharomyces
 CC cerevisiae to express the C. albicans ACCase gene in quantifiable
 CC amounts. Expression of the C. albicans ACCase gene in S. cerevisiae
 CC overcomes prior art problems of isolation and purification of the ACCase.
 CC Controlled overexpression is used to improve expression of the ACCase. It
 CC is possible to achieve about 14-fold overexpression relative to the wild-
 CC type host S. cerevisiae strain JK9-3D. This is achieved by replacing the
 CC C. albicans promoter in the expression construct by a stronger and
 CC preferably inducible promoter such as the S. cerevisiae GAL1 promoter
 XX
 SQ Sequence 2270 AA;

Query Match 70.9%; Score 2061.5; DB 2; Length 2270;
 Best Local Similarity 70.7%; Pred. No. 1.9e-183;
 Matches 390; Conservative 63; Mismatches 98; Indels 1; Gaps 1;
 QY 9 SQTGGNPLETAPASPVADFRKGGHVTIKVLCNNGIAAAYKEISIRKWAYETFGDE 68
 Db 70 SHFUGNSVLAEPKVRDFVRAHQGHVTSKILIANNGIAAAYKEISIRKWAYETFGDE 129
 QY 69 RAIEFTWMTPEDLKVNADYIRMAQVVEVPGGNNNNYANVDLIVDAERAGVHAWAG 128
 Db 130 KAIOFTWMTPEDLKVNADYIRMAQVVEVPGGNNNNYANVDLIVDAERAGVHAWAG 199

QY 129 WGHASNPRLPSLAASKHKIIPGPPGAMRSGLDKISSTIVAQHADVPCMPWSGTGIK 188
 Db 190 WGHASNPRLPSLAASKHKIIPGPPGAMRSGLDKISSTIVAQHADVPCMPWSGTGIK 249
 QY 189 ETWMSQ-GFLTYSDDVYQACHTAEGLKAEKIGYPVMIKASGGGGKIGKCTNGE 247
 Db 250 EVKIDPQTNLVSADDIYAKGCTSPEDGLEKAKKIGFPVMIKASGGGGKIGKVDDEK 309
 QY 248 EFKQLYNVLGEVPGSPVFMKLAGOARHLEVOLLADQYGNALISIFGRDCSVORRHQKII 307
 Db 310 NFITLYNQAAEIPGSPFIPMKLAGDARHLEVOLLADQYGNALISIFGRDCSVORRHQKII 369
 QY 308 EEPVTTIAPEDARESEKAAVRLAKLVGYVAGTVEWLYSPESGEPAFLELNPRLQVEHP 367
 Db 370 EEPVTTIAPEDARESEKAAVRLAKLVGYVAGTVEWLYSPESGEPAFLELNPRLQVEHP 429
 QY 368 TTEMVSGVNPAAQLQVAMGIPLYSIRSDIRTYLGMPPRGNEVIDDFSPSPSEKTKPKQ 427
 Db 430 TTEMVSGVNPAAQLQVAMGIPLYSIRSDIRTYLGMPPRGNEVIDDFSPSPSEKTKPKQ 489
 QY 428 PQGHVACRITAEVNPOTGPKPGMGALTELNFRSSTSTWYFVSGTSGALHEYADSFQHI 487
 Db 490 PKGHCTACRITSEDPCGEGFKPGSGSLHFNFRSSNNWYFVSGTSGALHEYADSFQHI 549
 QY 488 PAYGADRSEARKQWVLSIKELSIKSGDFRTTVEYLKLETDAPFNSKITTGWLDGLIQDR 547
 Db 550 FAFGENRQASRKHVVALKELSIKSGDFRTTVEYLKLETDAPFNSKITTGWLDGLIQDR 609
 QY 548 LTAERPPADLAV 559
 Db 610 LTAERPPADLAV 621

RESULT 8
 ADJ47654
 ID ADJ47654 standard; protein; 580 AA.
 XX
 AC ADJ47654;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE S. cerevisiae ACCase BC domain SEQ ID NO:8.
 XX
 DE ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
 KW biotin carboxylase domain; BC domain; fungicide.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN W02004013159-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 04-AUG-2003; 2003WO-US024356.
 XX
 PR 05-AUG-2002; 2002US-0401170P.
 XX
 PA (CROP-) CROPSOLUTION INC.
 XX
 PI Elich TD, Volrath SL, Weatherly SC;
 XX
 DR WPI; 2004-180421/17.
 XX
 PT Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
 PT biotin binding domain and carboxy transferase domain, and having
 PT functional biotin carboxylase domain, useful for identifying ACCase
 PT inhibitors/activators.
 XX
 PS Claim 9; SEQ ID NO 8; 56pp; English.
 XX
 CC The invention relates to a novel peptide (I) comprising an acetyl CoA
 CC carboxylase (ACCase) having a deleted biotin binding domain, having a
 CC deleted carboxy transferase domain, and having a functional biotin
 CC carboxylase domain. A peptide of the invention is useful for identifying

acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be a fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence represents an ACCase BC domain of the invention.

Sequence 580 AA;

Query Match	70.9%;	Score 2060;	DB 8;	Length 580;
Best Local Similarity	69.1%;	Pred. No. 2.6e-184;		

Qy	3	PHKAVSOFIGNPLETAPASVADFIRKOGGSHVITKVLI CNNGIAAAVKEIRSIRKWAY	62
Db	28	PGH-----FGLINTVDKLEESPLRDFVKSCHGGHTVISKILLI ANNGIAAAVKEIRSIRKWAY	82
Qy	63	ETFGDERALEFTWATPEDLKVNADYIRMAOVIEVPGGSNNNNYANVDLI VDVIAERAGV	122
Db	83	ETFGDGRITVQVAMATPDLLEANAEYIRMAOVIEVPGGTNNNNYANVDLI VDVIAERADV	142
Qy	123	HAVWAGWGHASENPRLPESLAASKHKHIFIGPPGSA MRS LGDKI SSTIVAOHADVPCKPW	182
Db	143	DAVWAGWGHASENPLLPKLSQSKKVI FIFPGPNAMRS LGDKI SSTIVAO SAKVPCIPW	202
Qy	183	SGTGKLTMTMSDO--GFLTVSDDVYQOACHTHTABEGLEKAEKIGYPMVI KASEGGGGRGI	240
Db	203	SGTGV-DTVHDEKTLGLVSDDDIYQKGCCTSPEDGLQAKRIGFPVMIKASEGGGGRGI	261
Qy	241	RKCTNGBEBFKOLYNALGEVPGSPVFMKLAGOARHLEVOLLADQVGNAI STFGRDCSVQ	300
Db	262	QVREEDFI IALYHOAANEIPGSPFI MKLAGARHLEVOLLADQVGTNTISUFGRDCSVQ	321
Qy	301	RRHOKIIEEAPVTITAPEDARESMEKAARLAKLVGVYSAGTVEWLYSPSGEGFAFLELNP	360
Db	322	RRHOKIIEEAPVTITAKAETHEMEKAARLVGLKLVGVYSAGTVEWLYSHDDGKFYLELNP	381
Qy	361	RLQVEHPPTMVSQVNI PAALQVAMGIPLYSIRDTIRTL YGMDPRGNEVIDPDFSPPSF	420
Db	382	RLQVEHPPTMVSQVNI PAALQLOI AMGIPMHRISDITRL YGMNPHSASEIDPEFKTQDAT	441
Qy	421	KTQRKPOQGHVACRITTAENPDTPFKPGMGALTELFNFSSTWGYSVGTSGALHEYA	480
Db	442	KKQRRPDKGHCTACRITSDPDNDGFPKSGGTLH LFNFSNNVMGYSVGNNGNIHSFS	501
Qy	481	DSQFGHIFAYGADRSEARKQWVLSKELSI RIGDFTTVEYLLKLETAFAFSNKITTTGWL	540
Db	502	DSQFGHIFAYGENRQASRKHVMVALKELSI RIGDFTTVEYLLKLETFEDFDNITTGWL	561
Qy	541	DGLIQDBLTABRRPADLAV	559
Db	562	DGLITHTOKTAEKDPDTLAV	580

RESULT 9

ABR52730

ID ABR52730 standard; protein: 2000 AA.

XX

AC XX

DT 20-JUN-2003 (first entry)
XX
DE Protein sequence #SEQ ID 325.
XX
KW Multiprotein complex; eukaryote; drug target; diagnosis.
XX
OS Saccharomyces cerevisiae.
XX
FN EP1258494-A1.
XX
PD
XX
XX 20-NOV-2002.
XX
XX 20-DEC-2001; 2001EP-00130253.
XX
XX 15-MAY-2001; 2001EP-00111774.
XX
XX (CELL-) CELLZOME AG.
XX
XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
PI Marzioch M, Schultz JD, Superti-Furga GD;
XX
XX WPI; 2003-250078/25.
DR
DR N-PSDB; ACC60772.
XX
XX New isolated protein complexes useful for diagnosing a disease or
PT disorder, or as a target for an active agent of a pharmaceutical,
PT preferably a drug target in the treatment or prevention of disease or
XX disorder.
PS Disclosure; SEQ ID NO 325; 17pp + Sequence Listing; English.
XX
XX The invention relates to multiprotein complexes from eukaryotes. Proteins
CC of the invention and DNA sequences encoding them are given in records
CC ABR52568-ABR53903 and ACC0610-ACC61944 respectively. The complexes are
CC obtainable by using a protein as a bait and isolating the set of proteins
CC which is attached thereto from cells. Such protein complexes may comprise
CC up to 30 distinct proteins. Protein complexes of the invention are useful
CC for diagnosing a disease or disorder, or as a target for an active agent
CC of a pharmaceutical, preferably a drug target in the treatment or
CC prevention of a disease or disorder. Note: The sequence data for this
CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM
XX
XX Sequence 2000 AA;
SQ

Qy	3	PDHKAVSQFTGGNPLETAPASPVPADFIRKOGHSHSVITKVLICNNGIAAIVKEIRSKWAY	62
Db	29	PGH-----PIGLNTVDKLESPRLDFVKSHGGHTVISKILLIANNGIAAIVKEIRSVRKWAY	83
Qy	63	ETFGDERATEFTWATPDEPKVNADYIRIMADQVIEVPGGSGNNNNYANVDLIVDVAERAGV	122
Db	84	ETFGDDRTVQVAMATPDELEANAEXYIRIMADQVIEVPGGTNNNNYANVDLIVDIAERADV	143
Qy	123	HAWACGWGHASENPRLPESIAASKHKIIIFGPPGSAMRSIGDKTSSITVAQHADVPCMPW	182
Db	144	DAWACGWGHASENPRLPEKLSQSQRKVIIFGPPGNAMRSIGDKTSSITVAQSAKVPICIPW	203
Qy	183	SGTGIKETWMSDQ--GFLTVDSDVYOQACITHTAEBGLEKAKEKIGYPWMIKASEGGGKGKI	240
Db	204	SGTGV-DTHVDEKTLGVSDDDIIYKGCCTSPEDGLQAKRIGFPWMIKASEGGGKGKI	262
Qy	241	RKCTNGEEPKQLYNAVIGBVPSPVFMKLAGOARHLEVLLADQYGNALISIFGRDCSVQ	300
Db	263	QVREEDFTALYHOAAEIPGSPFIMKLAGRARHLEVLLADQYGTNLSLFGDCSVQ	322
Qy	301	RRHQKIIIEAPVTIAPEDARESMEKAAVRIAKLVGVSAGTVEWLVSPPSGEFAFLELNP	360
Db	323	RRHQKIIIEAPVTIAKETHEMEKAAVRLKLVGVSAGTVEYLYSHDDCKYFFLELNP	382


```
XX 10-JAN-2003; 2003US-0439383P.
PR 31-MAR-2003; 2003US-0459464P.
PR 31-JUL-2003; 2003US-0451640P.
PR 27-OCT-2003; 2003US-0514636P.
PR 09-JAN-2004; 2004US-00514636.
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Tong L, Zhang H, Yang Z;
XX WPI; 2004-571486/55.
XX
XX New crystallizable composition comprising a carboxyltransferase domain of
PT acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, obesity,
PT cardiovascular disease, atherosclerosis, or cancer.
XX
XX Example 4; SEQ ID NO 1; 195pp; English.
XX
XX The invention comprises a crystallisable composition containing a
CC carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA)
CC carboxylase. The composition of the invention is useful for treating:
CC metabolic syndrome, diabetes, obesity, cardiovascular disease,
CC atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia,
CC hypertension, hyperuricaemia and renal dysfunction. The present amino
CC acid sequence represents a yeast acetyl-CoA carboxylase of the invention.
XX
XX Sequence 2233 AA;
XX
XX Query Match
XX Best Local Similarity 69.1%; Pred. No. 2.5e-183;
XX Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;
XX
XX 3 PDHKAISOQIGNPLETAPASPVADIRKOGGSHVITKVLICNNGIAAIVKIRSIKWAY 62
XX 29 PGH-----FIGLNTVDKLEESPLDFVKSHGGHTVISKILLIANNGLIAAIVKIRSVKWAY 83
XX
XX 63 ETFGDERAIEFTWATPEDLKNVADYIRWADOVEVPGGNNNNYANVDLIVDAERAGV 122
XX 84 ETFGDRTVQFVMAIPEDLEANAETIRWADOVIEVPGGTNNNNYANVDLIVDAERADV 143
XX
XX 123 HAVWAGWGHASENPRLPESLAASKHIIIFIGPPGSAMRSIGDKISSTIVAQAHDVPCMPW 182
XX 144 DAVWAGWGHASENPLLPKLSKRVIFIGPPGNAMRSIGDKISSTIVAQAQKVPICFW 203
XX
XX 183 SGTGKETWMSDQ--GFLTVDSDVYQACIHTAEBGLEKAEKIGYPMVIMKASEGGGKGI 240
XX 204 SGTGV-DTVHVDKTLVSDDDIYQKGCCTSPEDGLQAKRIGFPVIMKASEGGGKGI 262
XX
XX 241 RKTNGEEFKQLYNAVLPVGPSPVFMKLAGARHLEVOLLADQYGNATISFGRDSCVQ 300
XX 263 RQVEREEDFALYHQANEIPGPIFMKLAGARHLEVOLLADQYGTNIFLGRDCSVQ 322
XX
XX 301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGTVSAGTVEWLYSPESGEFAFLELNP 360
XX 323 RRHQKIIIEAPVTIAKAEFFHEMERAAVZLGLGVVSAGTVEYLYSHDDGFYFLELNP 382
XX
XX 361 RLOVEHPTTEMVSGVNPAAQLOVAMGPIYSIRDIRTLTYGMDPRGNEVIDFDFSPESF 420
XX 383 RLOVEHPTTEMVSGVNPAAQLOVAMGPIYSIRDIRTLTYGMDPRGNEVIDFDFSPESF 442
XX
XX 421 KTORPQPOGHVACRITAENPDTKFCMGALTELNFRSSSTWGYTSVGTSGALHYEA 480
XX 443 KQQRPIPKGHCTACRITSDPNDFGKPGGGTFLHNLFRSSSNVWGYTSVGNNGNIHFS 502
XX
XX 481 DSQFGHIFAYGADRSEARKQWISLKELSIKSGDFTTVEYLLKLETFAPESNKLTTGWL 540
XX 503 DSQFGHIFAYGADRSEARKQWISLKELSIKSGDFTTVEYLLKLETFAPESNKLTTGWL 562
XX
XX 541 DGLIQRDLTAERPPADLAV 559
XX 563 DDLITHKMTAEKPDPTLAV 591
```

RESULT 12

ADN19345
ID ADN19345 standard; protein; 2233 AA.

XX AC ADN19345;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #1998.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 1998; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition. Improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 2233 AA;

XX Query Match

70.9%; Score 2060; DB 8; Length 2233;

Best Local Similarity 69.1%; Pred. No. 2.5e-183; Matches 386; Conservative 76; Mismatches 89; Indels 8; Gaps 3;	
Qy	3 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAIVKEIRSKWA 62
Db	29 PGH-----FIGLTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAIVKEIRSVKWA 83
Qy	63 ETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGSGNNNNYANVDLIVDAEAGV 122
Db	84 ETFGDDRTVQVWATPEDLEANAAYIRMDQYIEVPGGTNNNNYANVDLIVDAEADV 143
Qy	123 HAVWAGHGHAENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAGHADVPCWP 182
Db	144 DAVWAGHGHAENRPLPEKLSQSKKVIIFIGPPGNAMRSLGDKISSIVVAQSAKVPICP 203
Qy	183 SGTGIGKTMMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPMVMIKASEGGGKGI 240
Db	204 SGTGV-DTVHVDKTLGLVSDVDIYQGCCTSPEDGLQAKRIGFPVMIKASEGGGKGI 262
Qy	241 RKTNGEFGKOLYNALVEVPGSPVFMVKLGAQARHLEVQLLADQYGNASIFGRDCSVQ 300
Db	263 QVEREEDFTALYHQAAANEIPGSPFITMKLAGRAHLEVQLLADQYGTNLSLGRDCSVQ 322
Qy	301 RRHQKIIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVVWLYSPESGEPAFLNLP 360
Db	323 RRHQKIIIEAPVTIATAETHEMEKAAVRLKLVGYVSAGTVVWLYSHDDGKFYFLNLP 382
Qy	361 RLQVEHPTTEMVSGVNPAAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDDFSPSEF 420
Db	383 RLQVEHPTTEMVSGVNLPAALQIANGIPMHRISDINTLYGNPHSAEIDFEKTDAT 442
Qy	421 KTORKPOGHVACRITAENPDTPGFGMGALTELNFRSTSTWGVFSVTSALHEYA 480
Db	443 KQORRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSNVWGVFSVGNNGNIHSF 502
Qy	481 DSQGHIFAYGADRSEARKOMVILKELSIKRGDPRFTTVEYLKLETDAPESNKITTGWL 540
Db	503 DSQGHIFAYGENRQARKMVAALKELSIKRGDPRFTTVEYLKLETFEDFEDNTITGWL 562
Qy	541 DGLIQDLRTAERPPADLAV 559
Db	563 DDLITHKMTAEKPDPTLAV 581
RESULT 13	
ID	ADN19252 standard; protein; 983 AA.
AC	ADN19252;
DT	02-DEC-2004 (first entry)
DE	Bacterial polypeptide #1905.
KW	Recombinant DNA construct; transformed plant; improved plant property;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW	pathogen tolerance; pest tolerance; plant disease resistance;
KW	cell cycle pathway modification; plant growth regulator;
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW	bacterial polypeptide.
OS	Bacteria.
XX	US2003233675-A1.
XX	18-DEC-2003.
XX	20-FEB-2003; 2003US-00369493.
XX	21-FEB-2002; 2002US-0360039P.
XX	(CAOY/) CAO Y.

PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
PI	CAO Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX	WPI; 2004-061375/06.
DR	
XX	
PT	New recombinant DNA construct comprising a promoter positioned to provide
PT	for expression of a polynucleotide encoding a polypeptide from a
PT	microbial source, useful for producing plants with improved properties.
XX	
PS	Claim 1; SEQ ID NO 1905; 122pp; English.
CC	The invention relates to a recombinant DNA construct comprising a
CC	promoter functional in a plant cell, where the promoter is positioned to
CC	provide for expression of a polynucleotide encoding a polypeptide from a
CC	microbial source. The invention also relates to a transformed plant
CC	comprising the recombinant DNA construct and a method of producing a
CC	transformed plant having an improved property. The plant is a crop plant
CC	such as maize or soybean. The method of producing a transformed plant
CC	having an improved property comprises transforming a plant with the
CC	recombinant DNA construct and growing the transformed plant, where the
CC	polynucleotide or polypeptide is useful for improving plant properties.
CC	The recombinant DNA construct is useful for producing plants with
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC	increased resistance to plant disease, better growth rate by modification
CC	of the cell cycle pathway with plant growth regulators, increased rate of
CC	homologous recombination, modified seed oil or protein yield and/or
CC	content, improved yield by modification of carbohydrate, nitrogen or
CC	phosphorus use and/or uptake, by modification of photosynthesis or by
CC	providing improved plant growth and development under at least one stress
CC	condition, improved lignin production or improved galactomannan
CC	production. This sequence represents a bacterial polypeptide used in the
CC	scope of the invention. Note: The sequence data for this patent did not
CC	form part of the printed specification but was obtained in electronic
CC	format from USPTO at seqdata.uspto.gov/sequence.html.
XX	
SQ	Sequence 983 AA;
Query Match 65.0%; Score 1889.5; DB 8; Length 983;	
Best Local Similarity 64.3%; Pred. No. 7.3e-168;	
Matches 355; Conservative 96; Mismatches 94; Indels 17; Gaps 4;	
Qy	2 PDHKAVSQFIGGNPLETAPASPVADFIKQGGHVSITKVLICNNGIAAIVKEIRSKWA 61
Db	105 PP-----QFIGLTVSSAQPSILRDFVLRGGHTVISKILIANNGIAAIVKEIRSKWA 158
Qy	62 YETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGSGNNNNYANVDLIVDAEAG 121
Db	159 YETFNDEKIIQFVVMATPDDLHANSEYIRMDQYVQVPGGTNNNNYANIDLIVDAEQTD 218
Qy	122 VHAVWAGHGHAENRPLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAGHADVPCMP 181
Db	219 VDAVWAGHGHAENRPLCPPELLASSQKILIFIGPPGRAMRSLGDKISSTIVAQSAKICIP 278
Qy	182 WSGTIGKTMMSDQ--GFLTVDSDVYQACIHTAEGLKAEKIGYPMVMIKASEGGGK 239
Db	279 WSGSHI-DTIHIDNKTNFVSPDDVYVVRGCGSSPEDALEKAKLIGFPVMIKASEGGGK 337
Qy	240 IRKCTNGEFGKOLYNALVEVPGSPVFMVKLGAQARHLEVQLLADQYGNASIFGRDCSV 299
Db	338 IRRVDNEDDFIALYRQAVNETPGSPMFMKVVTVDARHLEVQLLADQYGTNITLFGDCSI 397
Qy	300 ORRHOKIIIEAPVTIAPEDARESMKAAVRLAKLVGYVSAGTVVWLYSPESGEPAFLN 359
Db	398 ORRHOKIIIEAPVTIITKPTFQRMERAAIRLGLVGVNSAGTVVWLYSPKDDKFFYLELN 457
Qy	360 RLQVEHPTTEMVSGVNPAAQLQVAMGIPLYSIDRTLYGMDPRGNEVIDDFSPSES 419
Db	458 RLQVEHPTTEMISGVNLPATQIANGIPMHRISDIRKLYGLDPTGTSVID----- 509

QY 420 FKTORKPOGHVACRITAEINPTGPKPGMGALTELNFRSSTSTWGYFSGTSGALHEY 479
 DB 510 FKNLRPSGKHCISCRITSDPNEGPKPGTGKIHENFRSSNNVWGYFSGVNGAIHSF 569
 QY 480 ADSQFGHIFAYGADRSEARKQWISLKELSIKSGDFRITVEYLKLETDAPESNKITGW 539
 DB 570 SDSQFGHIFAVGNDQDAKQNVMLAKDPSIRGEFKPIEYILLELTRDPFESNNISTGW 629
 QY 540 LDGLIQDLRLTAE 551
 DB 630 LDDLILKNLSSD 641

RESULT 14
 ADK63986
 ID ADK63986 standard; protein; 2000 AA.
 AC ADK63986;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Disease treating protein complex-derived protein #1382.
 XX
 KW protein complex; drug target; diagnosis.
 XX
 OS Unidentified.
 XX
 PN EP1338608-A2.
 XX
 PD 27-AUG-2003.
 XX
 PF 20-DEC-2002; 2002EP-00102902.
 XX
 PR 20-DEC-2001; 2001EP-00130253.
 XX
 PA (CELL-) CELLZONE AG.
 XX
 PI Bauer A, Gavin A, Superti-Purga G, Kuester B, Schultz J;
 PI Marzloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK63987.

PT New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.

PS Disclosure; SEQ ID NO 2763; 13pp; English.

XX The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drug targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).

XX Sequence 2000 AA;

Query Match 65.0%; Score 1889.5; DB 7; Length 2000;
 Best Local Similarity 64.3%; Pred. No. 2.4e-167;
 Matches 355; Conservative .86; Mismatches 94; Indels 17; Gaps 4;
 QY 2 PPDHKAVSQFIGNPLETAPASVADPIRKGQGHSHVITKVLICNNGTAAVKEIRSTRKWA 61
 DB 105 PP-----QFIGNTVESQPSILRDFVLRGGHTVISKILIANNGTAAVKEIRSTRKWA 158
 QY 62 YETFGDERAIEFTVMTAPEDLVKNADYIRMDQYVEVPGSSNNNNYANVDLIYDVAERAG 121
 DB 159 YETFNDEKLIQFVVMATPDDLHANSEYIRMDQYVQVPGTNNNNYANIDLILDVAEQTD 218
 QY 122 VHAVWAGCHASENPRLPESLAASKHIIPIGPPGSAMRSLGDKISTTIVAQHADVPICMP 181
 DB 219 VDAVWAGWGHASENPCLPELLASSQSKILFIIGPPGRAMRSLGDKISTTIVAQSAKIPICP 278
 QY 182 WSGTGIGKETMMSDQ--GFLTVSDDVYQOACIHTABEGLEKAEKIGYPVVMIKASEGGGKG 239
 DB 279 WSGSHI-DTHIDNKTNFVSPDDVYVRCSSPEDALEKAKLIGFPVMIKASEGGGKG 337
 QY 240 IRKCTNGEEFKOLYNALGEVPGSPVFMKLAGQARHLEVQLLADQYGNASISIFGRDCSV 299
 DB 338 IRRVDNEDDFIALYRQAVNETPGSPMFMVVKVVTDAHLEVQLLADQYGTNITLFGDCSI 397
 QY 300 QRRHQIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEMLYSPESGEFAFLELN 359
 DB 398 QRRHQIIEEAPVTITKPTFQRMERAAIRLGLVGVVSAGTVLYSPKDDKFYLELN 457
 QY 360 PRLOVEHPTTEMVSGVNIIPAAOLOVAMGIPLYSIRDITRYLGMDDPRGNEVIDDFSPSPES 419
 DB 458 PRLOVEHPTTEMISGVNLPTATQIANGIPMHMISDIRKLYGLDPTGTSTVID----- 509
 QY 420 FKTORKPOGHVACRITAEINPTGPKPGMGALTELNFRSSTSTWGYFSGTSGALHEY 479
 DB 510 FKNLRPSGKHCISCRITSDPNEGPKPGTGKIHENFRSSNNVWGYFSGVNGAIHSF 569
 QY 480 ADSQFGHIFAYGADRSEARKQWISLKELSIKSGDFRITVEYLKLETDAPESNKITGW 539
 DB 570 SDSQFGHIFAVGNDQDAKQNVMLAKDPSIRGEFKPIEYILLELTRDPFESNNISTGW 629
 QY 540 LDGLIQDLRLTAE 551
 DB 630 LDDLILKNLSSD 641

RESULT 15

ADJ47655
 ID ADJ47655 standard; protein; 632 AA.
 XX
 AC ADJ47655;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human ACC1 BC domain SEQ ID NO:10.
 XX
 KW ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
 KW biotin carboxylase domain; BC domain; fungicide; human; ACC1.
 XX
 OS Homo sapiens.
 XX
 PN WO2004013159-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 04-AUG-2003; 2003WO-US024356.
 XX
 PR 05-AUG-2002; 2002US-0401170P.
 XX
 PA (CROP-) CROPSOLUTION INC.
 XX
 PI Elich TD, Volrath SL, Weatherly SC;
 XX
 DR WPI; 2004-180421/17.

XX Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
PT biotin binding domain and carboxyl transferase domain, and having
PT functional biotin carboxylase domain, useful for identifying ACCase
PT inhibitors/activators.
XX
PS Claim 9; SEQ ID NO 10; 56pp; English.
XX
CC The invention relates to a novel peptide (I) comprising an acetyl CoA
CC carboxylase (ACCase) having a deleted biotin binding domain, having a
CC deleted carboxyl transferase domain, and having a functional biotin
CC carboxylase domain. A peptide of the invention is useful for identifying
CC acetyl CoA carboxylase inhibitors or activators, which involves combining
CC the peptide and a compound to be tested for the ability to bind to the
CC biotin carboxylase domain, under conditions that permit binding to the
CC biotin carboxylase domain, determining whether or not the compound binds
CC to the biotin carboxylase domain, the presence of binding indicating the
CC compound is or may be an Acetyl CoA carboxylase inhibitor or activator.
CC The method further involves employing the identified binding compound in
CC an assay to detect inhibition or enhancement of Acetyl CoA carboxylase
CC activity, and selecting a compound that inhibits or activates Acetyl CoA
CC carboxylase activity. A peptide of the invention is also useful for
CC identifying fungicides, which involves combining the peptide and a
CC compound to be tested for the ability to bind to the biotin carboxylase
CC domain, under conditions that permit binding to the biotin carboxylase
CC domain, determining whether or not the compound binds to the biotin
CC carboxylase domain, the presence of binding indicating the compound is or
CC may be fungicide, employing the identified compound in an assay to detect
CC inhibition of Acetyl CoA carboxylase activity, and selecting a compound
CC that inhibits Acetyl CoA carboxylase activity. The present sequence
CC represents the human ACC1 BC domain.
XX
SQ Sequence 632 AA;

Query Match 61.6%; Score 1790; DB 8; Length 632;
Best Local Similarity 63.8%; Pred. No. 8.2e-159;
Matches 345; Conservative 79; Mismatches 103; Indels 14; Gaps 5;

QY 22 ASPVADPIRKGQSHSVITKVLICNGNIAAVKEIRSRKWAYETFGDERAIEFTVMATPED 81
DB 103 ASP-AEFVTRFGGKVKIEKVLIANNGIAAVKCMRSIRRSYEMFRNERAIRFVVMVTPED 161

QY 82 LKVNADYIRNADQYVEVPGSGNNNNYANVDLIVDVAERAGVAVWAGWGHASENPRLPES 141
DB 162 LKANAEYIRKADHVPVPGGNNNNYANVELLDIAKRIPVQAVWAGWGHASENPKLPEL 221

QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGKETWMSD---QGFL 198
DB 222 LL--KNGIAFMGPPSQAMWALGDKIASIVAQTAGIPTLPWSGSLRVQENDFSKRIL 279

QY 199 TVSDDVYQACIHTAEBGLEKAEKIGYPMIKASEGGGGKIRKCTNGEEFKQLYNAVLG 258
DB 280 NVFQELYKGVYKVDVLDGLKAAEBGVPMVIKASEGGGGKIRKVNADFPNLFQVQA 339

QY 259 EVPGSPVPMKLAGARHLEVOLLADQYGNASTFGEDCSVORHOKIEEAPVTTAPED 318
DB 340 EVPGSPVPMKLAGARHLEVOLLADQYGNASTFGEDCSVORHOKIEEAPVTTAPED 399

QY 319 ARESMKAAVRLAKLVGYVAGTVEWLYSPSEGEFAFLELNPRLOVHEPPTENVSGVNI 378
DB 400 VFEHMEQCAVKLAKMGVYVAGTVEYLYS-QDGSFFYLELNPRLOVHEPCTENVADNLP 458

QY 379 AAOQLVAMGIPLYSIRDIRTYLGYMDPRGNEVIDFSSPESFKTQKPPQGHVACRIT 438
DB 459 AAOQLVAMGIPLYRIKDIRMYGVSPMGDSPIPDFSA-----HVPCCPRGHVIAARIT 511

QY 439 AENPDGTFKFGMGALTELNFRSSTSTWGYFSGVGTSGALHEVDADQFQGHIFAYGADRSEAR 498
DB 512 SENPDEGFKPSSGTQVQELNFRSNKNWGYFSVAAGGLHEFADSQFGHCFSWGENREAI 571

QY 499 KQWISLKELSIKSGDFFTTVEYLYIKLLETDAFESNKITITGLDGLIQDLRTAERPPADLA 558
DB 572 SNNVVALKELSIKSGDFFTTVEYLYIKLLETESFQNNRIDTGLDGLIAEKVQAEPPDTMLG 631

QY 559 V 559
DB 632 V 632

RESULT 16

ADQ90744
XX ADQ90744 standard; protein; 2346 AA.
XX ADQ90744;
XX AC
XX DT 21-OCT-2004 (first entry)
XX DE Human acetyl-coenzyme A carboxylase - ACC1.
XX KW human; carboxyltransferase domain; CT domain;
KW acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase;
KW metabolic syndrome; diabetes; obesity; cardiovascular disease;
KW atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;
KW hypertension; hyperuricaemia; renal dysfunction;
KW crystallisable composition; enzyme; ACC1.
XX OS Homo sapiens.
XX PN WO2004063715-A2.
XX PD 29-JUL-2004.
XX PP 09-JAN-2004; 2004WO-US000585.
XX PR 10-JAN-2003; 2003US-0439383P.
XX PR 31-MAR-2003; 2003US-0459464P.
XX PR 31-JUL-2003; 2003US-0491640P.
XX PR 27-OCT-2003; 2003US-0514636P.
XX PR 09-JAN-2004; 2004US-00514636.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX QY Tong L, Zhang H, Yang Z;
XX WPI; 2004-571486/55.

New crystallisable composition comprising a carboxyltransferase domain of
acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, obesity,
cardiovascular disease, atherosclerosis, or cancer.

Example 4; SEQ ID NO 7; 195pp; English.

The invention comprises a crystallisable composition containing a
carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA)
carboxylase. The composition of the invention is useful for treating:
metabolic syndrome, diabetes, obesity, cardiovascular disease,
atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia,
hypertension, hyperuricaemia and renal dysfunction. The present amino
acid sequence represents a human acetyl-CoA carboxylase of the invention.

Sequence 2346 AA;

Query Match 61.5%; Score 1787; DB 8; Length 2346;
Best Local Similarity 63.6%; Pred. No. 1.4e-157;
Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

QY 22 ASPVADPIRKGQSHSVITKVLICNGNIAAVKEIRSRKWAYETFGDERAIEFTVMATPED 81
DB 103 ASP-AEFVTRFGGKVKIEKVLIANNGIAAVKCMRSIRRSYEMFRNERAIRFVVMVTPED 161

QY 82 LKVNADYIRNADQYVEVPGSGNNNNYANVDLIVDVAERAGVAVWAGWGHASENPRLPES 141
DB 162 LKANAEYIRKADHVPVPGGNNNNYANVELLDIAKRIPVQAVWAGWGHASENPKLPEL 221

QY 142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGKETWMSD---QGFL 198
DB 222 LL--KNGIAFMGPPSQAMWALGDKIASIVAQTAGIPTLPWSGSLRVQENDFSKRIL 279

Db 222 LL--KNGIAFMGPPSQMVALGDKIASSIVAQTAGITPLPWSGSLRVQNDPFSKRL 279
 QY 199 TVSDVVYQACIHTAEGLKAEKIGYPVMIKASEGGGKIGKCTNGEEFKOLYNALVG 258
 Db 280 NVPQELYEGYKVDVDDGLQAEEVGYPMIKASEGGGKIGKRVNADDPNLFQVQA 339
 QY 259 EYFGSPFVFMKLAGQARHLEVQLADQYGNALISFGKDCSVQRHOKIIEEAPVTIAPED 318
 Db 340 EYFGSPFVFMKLAGQARHLEVQLADQYGNALISFGKDCSVQRHOKIIEEAPVTIAPED 399
 QY 319 ARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 378
 Db 400 VFEHMEQCAVKLAKVGYVSAGTVEWLYS-QDGSFYFLELNPRLQVEHPTTEMVSGVNI 458
 QY 379 AAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDDFSSPESFKTQKPOGHVACRIT 438
 Db 459 AAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDDFSSPESFKTQKPOGHVACRIT 511
 QY 439 AENPDTGFKPGMGALTELFNRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498
 Db 512 SENPDEGFKPSSGTVQELNFRSNKNVGYFSAAGGLHEFAGSQFGHCFSGENREAI 571
 QY 499 KQWVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTTGWLGLQDRLTAEPPADLA 558
 Db 572 SNMVALKELSIKRGDFTTVEYLIKLETDAPESNKITTTGWLGLQDRLTAEPPADLA 631
 QY 559 V 559
 Db 632 V 632

RESULT 17

ID ABP70270 standard; protein; 2346 AA.
 AC ABP70270;
 DT 07-APR-2003 (first entry)
 DE Amino acid sequence of human acetyl coenzyme A-carboxylase alpha.
 KW Acetyl coenzyme A-carboxylase alpha; ACC-alpha; BRCA1; breast cancer;
 KW ovarian cancer.
 OS Homo sapiens.
 PN WO2002100897-A2.
 PD 19-DEC-2002.
 PP 12-JUN-2002; 2002WO-FR002016.
 PR 13-JUN-2001; 2001FR-00007740.
 PR 05-MAR-2002; 2002FR-00002789.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (UCLY-) UNIV LYON 1 BERNARD CLAUDE.
 PI Dalla Venezia N, Magnard C, Lencir G, Sinilnikova-Brard O;
 DR WPI; 2003-148772/14.
 DR N-PSDB; ABZ23503.

New molecular complex of BRCA1 protein and acetyl coenzyme A-carboxylase alpha, useful in screening agents suitable for treatment, prevention or diagnosis of cancer.

Disclosure; Page 55-62; 62pp; French.

The present sequence represents human acetyl coenzyme A-carboxylase alpha (ACC-alpha). The ACC-alpha protein was used in the course of the invention. The specification describes a molecular complex comprising a polypeptide having amino acids 1640-1663 of the human BRCA1 protein (or

similar sequence from some other animal species), and a polypeptide that is a part of the acetyl coenzyme A-carboxylase alpha (ACC-alpha) protein able to bind the BRCA1 protein. The complex is implicated in predisposition to cancer of breast and ovary. It is used to screen for compounds that modulate interaction between BRCA1 and ACC-alpha, which are potentially useful for treatment, prevention and diagnosis of cancer, and to identify endogenous ligands. Modulated formation of the complex can be used for diagnosis of cancer. Antibodies directed against specific parts of human ACC-alpha are useful for localization of the complex in cells

Sequence 2346 AA;

Query Match 61.3%; Score 1781; DB 6; Length 2346;

Best Local Similarity 63.6%; Pred. No. 5.2e-157;

Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

QY 22 ASPVADPFRKGGHSHVITKVLICNNGIAAVERISIRKWAYETFGDERALETWATPED 81
 Db 103 ASP-ABFVTRFGGNKVIKVLINNGIAAVERISIRKWAYETFGDERALETWATPED 161
 QY 82 LKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHAVWAGHASENRLPES 141
 Db 162 LKANAAYIKMADHYVPVPGGANNNNYANVELLDIAKRIPIQAVWAGHASENPKLP 221
 QY 142 LAASKHKIIFIPGPGSAMSISGDKISSTIVAHADVPCWPSGTGKETMMSD---QGFL 198
 Db 222 LL--KNGIAFMGPPNQAMWALGDKIASSIVAQTAGITPLPWSGSLRVQNDPFSKRL 279
 QY 199 TVSDVVYQACIHTAEGLKAEKIGYPVMIKASEGGGKIGKCTNGEEFKOLYNALVG 258
 Db 280 NVPQELYEGYKVDVDDGLQAEEVGYPMIKASEGGGKIGKRVNADDPNLFQVQA 339
 QY 259 EYFGSPFVFMKLAGQARHLEVQLADQYGNALISFGKDCSVQRHOKIIEEAPVTIAPED 318
 Db 340 EYFGSPFVFMKLAGQARHLEVQLADQYGNALISFGKDCSVQRHOKIIEEAPVTIAPED 399
 QY 319 ARESMEKAARLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 378
 Db 400 VFEHMEQCAVKLAKVGYVSAGTVEWLYS-QDGSFYFLELNPRLQVEHPTTEMVSGVNI 458
 QY 379 AAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDDFSSPESFKTQKPOGHVACRIT 438
 Db 459 AAQLQVAMGIPLYSIRDTLYGMDPRGNEVIDDFSSPESFKTQKPOGHVACRIT 511
 QY 439 AENPDTGFKPGMGALTELFNRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498
 Db 512 SENPDEGFKPSSGTVQELNFRSNKNVGYFSAAGGLHEFAGSQFGHCFSGENREAI 571
 QY 499 KQWVLSKELSIKRGDFTTVEYLIKLETDAPESNKITTTGWLGLQDRLTAEPPADLA 558
 Db 572 SNMVALKELSIKRGDFTTVEYLIKLETDAPESNKITTTGWLGLQDRLTAEPPADLA 631
 QY 559 V 559
 Db 632 V 632

RESULT 18

ID ABP59197 standard; protein; 2346 AA.

AC ABP59197;

DT 01-MAY-2003 (first entry)

DE Human acetyl-Coenzyme A-carboxylase-alpha variant #1.

KW Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer; breast; ovary.

OS Homo sapiens.

QY 199 TVSDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNAVVLG 258
 DB 280 NVPQELYEKGVKVDVDDGLKAEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNAVVLG 339
 QY 259 EYVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIIEEAPVTIAPED 318
 DB 340 EYVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIIEEAPVTIAPED 399
 QY 319 ARESMEKAAVRLAKLVGVSAGTVEWLYSPSGGFAPLELNPRLQVEHPTTEMVSGVNIP 378
 DB 400 VFEHMEQCAVLAQKMGVVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVSGVNIP 458
 QY 379 AAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTKRQPOGHVACRIT 438
 DB 459 AAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTKRQPOGHVACRIT 511
 QY 439 AENPDTPGKPGMGALTELNFRSSTSTMGYFSGVSGALHEVADSFQGHIFAYGADRSEAR 498
 DB 512 SENPDGFKPSSGTVOELNFRSNKNVGYFSAAGGLHEFAGSGFCHCSWGENREEAI 571
 QY 499 KQWISLKELSIRGDFRTTVEYLYLKLETDAPESNKITTTGWLGLIQRDLTAERPPADLA 558
 DB 572 SNMVVALKELSIKRGDFRTTVEYLYLKLETDAPESNKITTTGWLGLIQRDLTAERPPADLA 631
 QY 559 V 559
 DB 632 V 632

RESULT 20

ABP59198
 ID ABP59198 standard; protein; 2346 AA.

AC ABP59198;
 DT 01-MAY-2003 (first entry)

XX Human acetyl-Coenzyme A-carboxylase-alpha variant #2.
 DE Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;
 XX Human; breast; ovary.
 KW Homo sapiens.

OS Key Location/Qualifiers
 FH Misc-difference 2271 /note="Ala substituted with Val"
 FT WO2002100896-A2.
 XX 19-DEC-2002.
 PD 12-JUN-2002; 2002WO-FR002015.
 XX 13-JUN-2001; 2001FR-00007740.
 PR 05-MAR-2002; 2002FR-00002788.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.

XX Dalla Venezia NL, Magnard CM, Lenoir GM, Sinilnikova-Erard O;
 XX WPI; 2003-175165/17.
 DR In vitro diagnosis of cancer, particularly breast and ovarian cancer, or
 PT susceptibility, comprises detecting alterations in the acetyl coenzyme A-
 PT carboxylase alpha gene or protein expression.
 XX Example 2; Page; 56pp; French.
 PS The present sequence is a variant sequence for human acetyl-Coenzyme A-
 CC carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro

CC diagnosis of cancer (or of an increased risk of developing it), by
 CC detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha
 CC protein expression, relative to a control population. The method is
 CC particularly used to diagnose cancer, especially of breast or ovary, or
 CC for assessing the risk of developing such cancers. Note: The present
 CC sequence was not shown in the specification, but was derived from
 CC information given

XX SQ Sequence 2346 AA;

Query Match 61.3%; Score 1781; DB 6; Length 2346;
 Best Local Similarity 63.6%; Pred. No. 5.2e-157;
 Matches 344; Conservative 79; Mismatches 104; Indels 14; Gaps 5;

QY 22 ASPVADPIRQGGHSHVITKVICNNGIAAVKBIKIRKWAYETFGDERAIEFTVMATPED 81
 DB 103 ASP-AEFVTRFGCKVIEKVLIANGLAAVKCRSIRRSYENFRERAIRFVVMVTPED 161
 QY 82 LKYNADYIRMDQYVEVPGSSNNNTANVDLIVDVAERAGVHAWAGWGHASENPRLPES 141
 DB 162 LKANAAYIKMADHYVPVPGANNNTANVELIILDAKRIIPVQAVWAGWGHASENPRLPES 221
 QY 142 LAASKHKIIFIGPPGAMBSLGDKISSTIVAOHADVPCHPWSCTGIGKETWMSD---QGFL 198
 DB 222 LL--KNGIAFMGPPNQMMALGDKIASISVAQTAGIPTLPWSGSLRVVDWQENDFSKRIL 279
 QY 199 TVSDVYQACIHTAEGLKAEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNAVVLG 258
 DB 280 NVPQELYEKGVKVDVDDGLKAEKIGYPMIKASEGGGKGIRKCTNGEEFKQLYNAVVLG 339
 QY 259 EYVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIIEEAPVTIAPED 318
 DB 340 EYVPGSPVFMKLAGQARHLEVQLLADQYGNALISIFGRDCSVORRHQKIIEEAPVTIAPED 399
 QY 319 ARESMEKAAVRLAKLVGVSAGTVEWLYSPSGGFAPLELNPRLQVEHPTTEMVSGVNIP 378
 DB 400 VFEHMEQCAVLAQKMGVVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPTTEMVSGVNIP 458
 QY 379 AAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTKRQPOGHVACRIT 438
 DB 459 AAQLQVAMGIPLYSIRDIRTYLGMDCPRGNEVIDFDFSSPESFKTKRQPOGHVACRIT 511
 QY 439 AENPDTPGKPGMGALTELNFRSSTSTMGYFSGVSGALHEVADSFQGHIFAYGADRSEAR 498
 DB 512 SENPDGFKPSSGTVOELNFRSNKNVGYFSAAGGLHEFAGSGFCHCSWGENREEAI 571
 QY 499 KQWISLKELSIRGDFRTTVEYLYLKLETDAPESNKITTTGWLGLIQRDLTAERPPADLA 558
 DB 572 SNMVVALKELSIKRGDFRTTVEYLYLKLETDAPESNKITTTGWLGLIQRDLTAERPPADLA 631
 QY 559 V 559
 DB 632 V 632

RESULT 21

ABP59490
 ID ABP59490 standard; protein; 2348 AA.

XX ABP59490;
 AC ABP59490;

XX 26-MAR-2002 (first entry)
 DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 5262.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmacological.

XX Drosophila melanogaster.
 OS Drosophila melanogaster.

XX WO200171042-A2.
 XX 27-SEP-2001.


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Db 470 GIPYRLKDIRLLYGESPMGSSVIDFE-----NPPNKRPSGHVIAARITSENDEGF 522
QY 447 KPGMGALTELNFRRSTSTWGYFSGVTSGALHEYADSFQGHIPAYGADRSEARKQWISLK 506
Db 523 KPSGTVQELNFRSSKNVWGYFSAASGLHEFADSFQGHCFSGWGENRQQAENLVIALK 582
QY 507 ELSIRGDFRTTVEYLIKLLETDAPESNKITTTGWLGLIQDLRTAERPPADLAV 559
Db 583 ELSIRGDFRTTVEYLIKLLETNFLDINSIDTAWLDALIAERVOSEKPDILLGV 635

RESULT 23
ABB83866
ID ABB83866 standard; protein; 2348 AA.
XX
AC ABB83866;
XX
DT 04-OCT-2002 (first entry)
XX
DE Drosophila melanogaster ACCase SEQ ID NO 2.
XX
KW Drosophila melanogaster; fruit fly; Acetyl-CoA carboxylase; ACCase;
KW insecticide; acaricide; EC 6.4.1.2; enzyme.
XX
OS Drosophila melanogaster.
XX
PN DE10062421-Ai.
XX
PD 20-JUN-2002.
XX
PF 14-DEC-2000; 2000DE-01062421.
XX
PR 14-DEC-2000; 2000DE-01062421.
XX
PA (FARB ) BAYER AG.
XX
PI Franken E, Nauen R, Teuschel U;
XX
WPI; 2002-584630/63.
DR N-PSDB; ABB85738.
XX
New nucleic acid encoding insect acetyl-coenzyme A carboxylase, useful
PT for identifying insecticidal and acaricidal agents, also related proteins
PT and modulators.
XX
PS Claim 8; Page 21-27; 34pp; German.
XX
The invention relates to a novel nucleic acid (I) comprising (i) a 4047
CC bp sequence (ABB85738) or AAF59156; (ii) a segment with at least 14 bp
CC from (i); (iii) a sequence that hybridizes to (i) or (ii) at 37-50°C;
CC (iv) a sequence at least 60% identical with (i) or (ii); (v) a complement
CC of (i)-(iv) or (vi) an equivalent of (i)-(iv) within the degeneracy of
CC the genetic code. (I) and the encoded polypeptide (II, ABB83866) having
CC ACCase (acetyl-CoA carboxylase, EC 6.4.1.2) activity are used to identify
CC insecticidal and acaricidal agents that act by modulating activity or
CC expression of ACCase, an essential enzyme for survival of insects. The
CC present sequence is that of the Drosophila melanogaster ACCase of the
CC invention
XX
Sequence 2348 AA;

Query Match 61.2%; Score 1780; DB 5; Length 2348;
Best Local Similarity 64.2%; Pred. No. 6.5e-157;
Matches 342; Conservative 69; Mismatches 110; Indels 12; Gaps 4;

QY 27 DFRKGGHSHVITKVLICNNGIAAVKEIRSIKWAYETFGDERAIEFTVMATPEOLKYNA 86
Db 115 EFVKRFGGTRVINKVLIANNGLAAVKMKRSIRWAYEMFKNERAIRFVVMVTPEDLKANA 174
QY 87 DYIRMADQVVEPFGSSNNNNYANVDLIVDAERAGVHVAWAGHGHASENRPPLPESLAASK 146
Db 175 EYIKWADHYVPVPGSSNNNNYANVELIVDIALRTQVQVWAGHGHASENPKPELL--HK 232

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QY 147 HKIIFGPGSAMRSIGDKISSTIVQAHDVPCMPWSGTGIKETMMSDQGLFTVSDVYQ 206
Db 233 EGLVFLGPPERANWALGDKVASSIVAQTAEIPTLPWSGSDLKAQYSGKK--IKISSELP 290
QY 207 QACIHTABEGLEKAEKIGYPVMIKASEGGGGKIRKCTNGEBFKOLYNALVGEVPGSPVP 266
Db 291 RGCVTNVEGLAAVNKIGFPVMIKASEGGGGKIRKCTNGEBFKOLYNALVGEVPGSPVP 350
QY 267 VMKLAGARHLEVLQADQYGNASIFGRDCSVQRHOKIIEEAPVTIAPEDARESMEXA 326
Db 351 VMKLAGARHLEVLQADQYGNASIFGRDCSVQRHOKIIEEAPVAIQAPEVFEDEMEXA 410
QY 327 AVRLAKLYGVYSAGTVEMLYSPESGEFAPLEINPLQVEHPHTEMVSGVNIIPAAQLQVAM 386
Db 411 AVRLAKMVGYSAGTVEMLYDPE-GRYFFLELNPRLQVEHPHTEMVADVNLPAALQIQGM 469
QY 387 GIPLYSIIRDITLYGMDPRGNEVIDFDSSPSFQTKRQPOGHVACRIITAENPDTCF 446
Db 470 GIPLYRLKDIRLLYGESPMGSSVIDFE-----NPPNKRPSGHVIAARITSENDEGF 522
QY 447 KPGMGALTELNFRRSTSTWGYFSGVTSGALHEYADSFQGHIPAYGADRSEARKQWISLK 506
Db 523 KPSGTVQELNFRSSKNVWGYFSAASGLHEFADSFQGHCFSGWGENRQQAENLVIALK 582
QY 507 ELSIRGDFRTTVEYLIKLLETDAPESNKITTTGWLGLIQDLRTAERPPADLAV 559
Db 583 ELSIRGDFRTTVEYLIKLLETNFLDINSIDTAWLDALIAERVOSEKPDILLGV 635

RESULT 24
AAB86033
ID AAB86033 standard; protein; 2288 AA.
XX
AC AAB86033;
XX
DT 13-JUL-2001 (first entry)
XX
DE Bovine acetyl-coenzyme A carboxylase-alpha protein fragment.
XX
KW Acetyl-coenzyme A carboxylase-alpha; acetyl-coA carboxylase alpha;
KW bovine; milk gland-specific promoter; Accalpha; milk production; sheep;
KW goat; fat content; genotyping; lactation.
XX
OS Bos taurus.
XX
PN DE19946173-A1.
XX
PD 05-APR-2001.
XX
PF 20-SEP-1999; 99DE-01046173.
XX
PR 20-SEP-1999; 99DE-01046173.
XX
PA (BIOL-) FORSCHUNGSINSTITUT BIOLOGIE LANDWIRTSCHA.
XX
PI Seyfert HM;
XX
DR WPI; 2001-258968/27.
DR N-PSDB; AAF88002.
XX
New nucleic acid encoding bovine acetyl coenzyme A carboxylase alpha and
PT its promoter, for milk-specific production of proteins and for regulating
PT fat content of milk.
XX
Claim 2c; Page 24-30; 44pp; German.
XX
This invention describes a novel milk gland-specific promoter of the
CC bovine acetyl coenzyme A carboxylase alpha gene (Accalpha), or its
CC fragments, which are used to control expression of foreign genes. When
CC the promoter (or the Accalpha structural gene) is replaced, at least in
CC part, by a sequence that is altered by deletion or substitution, then
CC expression of Accalpha in the milk gland is reduced and the milk produced

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XX AC ABM83569;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3818.
 XX DT 12-SEP-2002; 2002US-0410259P.
 XX PR 12-SEP-2002; 2002US-0410260P.
 XX PA (INCY-) INCYTE CORP.
 XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Harthehorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV, Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH, Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patury S, Shi X, Suarez CJ;
 XX WPI: 2004-329368/30.
 XX DR N-PSDB; ACN42221.
 XX DT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
 XX PS Claim 27; Page; 190pp; English.
 XX CC The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorder, gastrointestinal disorder, endocrine infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX SQ Sequence 2420 AA;
 XX Query Match 60.9%; Score 1769.5; DB 8; Length 2420;
 XX Best Local Similarity 63.4%; Pred. No. 6.6e-156;
 XX Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;
 QY 22 ASPVADFKRQGGHSHVITKVLICNNGIAAVKIRSKWAYETFGDERAIEFTVMATPED 81
 DB 245 ASP-AEFVTRFGDRVIEKVLINNGIAAVKCRSIRWAYENFRNRAIRFVWMTPED 303
 QY 82 LKVNADYIRMDQYVEYFGSGNNNNYANVDLIVDAERAGVHAVWAGHASENRLPES 141
 DB 304 LKANAAYIKWADHYVPVPGPNNNYANVELIVDIKRIPIQVAVWAGHASENKLPEL 363
 QY 142 LAASKHKIIFITGPGSMRSLGDKISSTIVAOHADVPQCMPSWGTGKETMMSD---QG-F 197

Db 364 LC--KNGVAPLGGPSEAMWALGDKIASTVVAQTLOVPTLPWSGSLTVEWTTDLQGGKR 421
 QY 198 LTVSDDDVYQOACIHTAEGLKAEKIGYPWMIKASGGGGKGIKCTNGEEFKQLYNVL 257
 Db 422 ISVPEDVYDKGCKVDDEGLEAAERIGFPLMIKASGGGGKGIKKAESAEDFFILFRVQ 481
 QY 258 GEVPGSPFVFMKLAGOARHLEVLQADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPE 317
 Db 482 SETPGSPFIFLMKLAQARHLEVLQADQYGNALISIFGRDCSVQRRHQKIEEAPVTIAPE 541
 QY 318 DARESMEKAAVRLAKLVGVVSAGTVEWLYSPESGGEFAFLELNPRLQVEHPTTEKVSQNI 377
 Db 542 AIFERMEQCAIRLAKTVGVVSAGTVEWLYS-QDGSFHFLELNPRLQVEHPTTEKVSQNI 600
 QY 378 PAAQLQVAMGIPLYSIRDIRTLTYGMDPRGNEVIDDFDSSPESPKT-QRKPPQPGHVACR 436
 Db 601 PAAQLQVAMGIPLYSIRDIRTLTYGMDPRGNEVIDDFDSSPESPKT-QRKPPQPGHVACR 652
 QY 437 ITAENPDTGFKPGMGALTELNFRRSSTTWGYSVGTSGALHEYADSQFGHIFAYGADRSE 496
 Db 653 ITSENPDGFKPSSGTVQELNFRSSKNVWGVSVAAATGGLHREFADSQFGHIFAYGADRSE 712
 QY 497 ARKQWISLSELSIRGDFRTTVEYLKLETTAFESNKTITGWLGLIQRLTAERPPAD 556
 Db 713 AISNMVVALKELSGRDFRTTVEYLKLETTAFESNKTITGWLGLIQRLTAERPPAD 772
 QY 557 LAV 559
 Db 773 LGV 775
 RESULT 27
 ABP59211
 ID ABP59211 standard; protein; 2458 AA.
 XX AC ABP59211;
 XX DT 10-MAY-2003 (first entry)
 XX DE Human drug metabolising enzyme, DME-2, SEQ ID 2.
 KW Human; drug metabolising enzyme; anti-HIV; antiallergic;
 KW antinflammatory; antianaemic; thrombolytic; antilipaeamic; antidiarrheic;
 KW antiarteriosclerotic; antiasthmatic; immunosuppressive; antichyroid;
 KW cytostatic; hepatotropic; virucide; dermatological; antidiabetic;
 KW nephrotropic; angiotropic; neuroprotective; thymimetic; osteopathic;
 KW antiarthritic; antipeoriatic; uropathic; ophthalmological; antirheumatic;
 KW haemostatic; gene therapy; cell proliferative disorder; cancer;
 KW developmental disorder; endocrine disorder; eye disorder;
 KW metabolic disorder; gastrointestinal disorder; liver disorder;
 KW autoimmune disorder; inflammatory disorder; DME-2.
 OS Homo sapiens.
 XX WO2003004608-A2.
 XX PD 16-JAN-2003.
 XX PF 05-JUL-2002; 2002WO-US0211105.
 XX PR 06-JUL-2001; 2001US-0303745P.
 XX PR 13-JUL-2001; 2001US-0305402P.
 XX PR 27-JUL-2001; 2001US-0308158P.
 XX PR 14-SEP-2001; 2001US-0322127P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Griffin JA, Ramkumar J, Emerling BM, Richardson TW, Li JX,
 PI Warren BA, Honchell CD, Baughn MR, Tang YT, Lee EA, Elliott VS,
 PI Yue H, Lee S, Swarnakar A, Forsythe LJ, Sanjanwala MM, Yao MG,
 PI Zebartjadian Y, Gorvad AB, Becha SD, Burford N;


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PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX (CURA-) CURAGEN CORP.
XX
XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Carterton E, Burgees C, Leite M, Zhong H, Alsbrook JP;
PI Lepley DM, Rieger DK;
XX
XX WPI; 2002-723332/78.
DR N-PSDB; ABX97116.
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
XX Claim 1; Page 313-314; 1103pp; English.
XX
XX This invention describes novel human NOVX polypeptides which have
CC cystostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. AB065041-AB065218 represent the NOVX polypeptides encoded by
CC ABX97008-ABX97185
XX
XX Sequence 2498 AA;
XX
XX Query Match 60.9%; Score 1769.5; DB 5; Length 2498;
XX Best Local Similarity 63.4%; Pred. No. 7e-156;
XX Matches 344; Conservative 75; Mismatches 107; Indels 17; Gaps 7;
XX
XX 22 ASPVADFRKGGHSHVIFKVLICNNGIAAVERISIRKWAYETFGDERAIEFTVMATPED 81
XX 235 ASP-AEFVTRGGDRVIEKVLINNGIAAVERISIRKWAYEMFNERAIRFVVMATPED 293
XX
XX 82 LKVNADYIRMDQYVEYVPGSGNNNNYANVDLIVDAERAGVHVAWAGHASENPRLPES 141
XX 294 LKANAERYIKMADHYVPVPGSGNNNNYANVELIVDAIKRIPVOAVWAGHASENPRLPEL 353
XX
XX 142 LAASKHKLIFIPGCSAMRSIGDKISITVAQHADVPCMPHSGTGIKETWMSD---QG-F 197
XX 354 LC--KNGVAFILGPPSEAWWALGDKIASTVVAQTQVPTLPWSSGSLTVETEDDLQOQKR 411
XX
XX 198 LTVSDVYQACIHTAEGLKAEKIGYPMVKASEGGGGKIRKCTNGEEFKOLYNVAVL 257
XX 412 ISVEDVYDKGVKVDGDELAERIGFPLMKASEGGGGKIRKAEADFFILFRQVQ 471
XX
XX 258 GEVPGSPVFMKLAQAPHLVQLADQYNAISIFGRDCSVQRHOKIIEAPVTIAPE 317
XX 472 SEIPGSPFLMKLAQHARHLEVLQADQYNAVSLFGRDCSVQRHOKIIEAPVTIAPE 531
XX
XX 318 DARESMKAAVRLAKLVGVYAGTVMWLYSPESGEPAFLNPLRLOVEHPTEMVSGVNI 377
XX 532 AIFEFMEQCAIRLAKTVGVYAGTVMWLYS-QDGSFHELNPLRLOVEHPCTEMIAVNL 590
XX
XX 378 PAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVIDFDPSSPESFKT-QRKPOQGVWACR 436
XX 591 PAAQLQVAMGIPLYSIRDTIRLYGMDPRGNEVIDFDPSSPESFKT-QRKPOQGVWACR 642
XX
XX 437 ITAENPDGFKPGMGALTELFNRSTSTWGYFSGVTSGLAHYADSQFGHIFAYCADRSE 496
XX 643 ITSENPDGFKPGMGALTELFNRSTSTWGYFSGVTSGLAHYADSQFGHIFAYCADRSE 702
XX
XX 497 ARKQWVLSKELSGIRGDRFTTVEYLILKLETDAPESNKITTTGWLGLDGLITAEPRPAD 556
XX
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Db 703 AISNMVVALKELSGIRGDRFTTVEYLILKLETDAPESNKITTTGWLGLDGLITAEPRPADIM 762
QY 557 LAV 559
Db 763 LGV 765

RESULT 30
ADN61949
ID ADN61949 standard; protein; 2498 AA.
XX
XX ADN61949;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human novel protein NOV76a.
DE
XX
XX Human; NOVX; diabetes; obesity; infectious disease; anorexia;
XX cancer-associated cachexia; cancer; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; immune disorder;
XX haematopoietic disorder; dyslipidaemia; chronic disease.
XX
XX Homo sapiens.
OS
XX
XX US2004043382-A1.
XX
XX 04-MAR-2004.
PD
XX
XX 07-MAR-2002; 2002US-00092900.
PF
XX
XX 08-MAR-2001; 2001US-0274191P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275378P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 28-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281444P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
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ADJ47656;
06-MAY-2004 (first entry)
Human ACC2 BC domain SEQ ID NO:12.
ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
biotin carboxylase domain; BC domain; fungicide; human; ACC2.
Homo sapiens.
W02004013159-A2.
12-FEB-2004.
04-AUG-2003; 2003WO-US024356.
05-AUG-2002; 2002US-0401170P.
(CROP-) CROPSOLUTION INC.
Elich TD, Volrath SL, Weatherly SC;
WPI; 2004-180421/17.
Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
biotin binding domain and carboxy transferase domain, and having
functional biotin carboxylase domain, useful for identifying ACCase
inhibitors/activators.
Claim 9; SEQ ID NO 12; 56pp; English.
The invention relates to a novel peptide (I) comprising an acetyl CoA
carboxylase (ACCase) having a deleted biotin binding domain, having a
deleted carboxy transferase domain, and having a functional biotin
carboxylase domain. A peptide of the invention is useful for identifying
acetyl CoA carboxylase inhibitors or activators, which involves combining
the peptide and a compound to be tested for the ability to bind to the
biotin carboxylase domain, under conditions that permit binding to the
biotin carboxylase domain, determining whether or not the compound binds
to the biotin carboxylase domain, the presence of binding indicating the
compound is or may be an Acetyl CoA carboxylase inhibitor or activator.
The method further involves employing the identified binding compound in
an assay to detect inhibition or enhancement of Acetyl CoA carboxylase
activity, and selecting a compound that inhibits or activates Acetyl CoA
carboxylase activity. A peptide of the invention is also useful for
identifying fungicides, which involves combining the peptide and a
compound to be tested for the ability to bind to the biotin carboxylase
domain, under conditions that permit binding to the biotin carboxylase
domain, determining whether or not the compound binds to the biotin
carboxylase domain, the presence of binding indicating the compound is or
may be fungicide, employing the identified compound in an assay to detect
inhibition of Acetyl CoA carboxylase activity, and selecting a compound
that inhibits Acetyl CoA carboxylase activity. The present sequence
represents the human ACC2 BC domain.
Sequence 774 AA;
Query Match 59.8%; Score 1738; DB 8; Length 774;
Best Local Similarity 62.8%; Pred. No. 9.1e-154;
Matches 341; Conservative 76; Mismatches 106; Indels 18; Gaps 8;
22 ASPVADPIKGGSHVITKVLICNGIAAIVKVEIRSIKWAYETFGDRAIEFTVMATPED 81
245 ASP-AEFTVTRFGGDRVIEKVLIAANGIAAIVKVEIRSIKWAYETFGDRAIEFTVMATPED 303
82 LKYNADYIRWADOVEYVPGSSNNNNYANDLIVDVAERAGVHAWAGMGHASENPLRPES 141
304 LKNAEYIKWADHYVVPVPGPNNNNNYANVLLVIAKRIPLQAVWAGMGHASENPKLP 363
142 LAASKKHIIIFIGPGSAMSILGDKISSTIVAQHADVPCMPWMSGTGKETWMSD---QG-F 197
364 LC--KNGVAFGLPSPSEAWALGDKIASTVVAQTLOVTLPRSGSLTVENTEDDLOQGR 421

QY 198 LTVSDVYQACIHTAEGLKAEKIGYPMIKASGGGGKGIKCTNGEEFKQLYNVL 257
DB 422 ISVPEDVYDKGCVKQVDEGLEAERIGFPLMIKASGGGGKGIKCAESAEDFPILFRVQ 481
QY 258 GRVPGSPVFMKLAGOARHLEVOLLADQYGNASISIFGRDCSVORRHOKIIEEAPVTIAPE 317
DB 482 SIIPSPFIPLMKLAQARHLEVOLLADQYGNASISIFGRDCSVORRHOKIIEEAPVTIAPE 541
QY 318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPSGSFBFALELNPRLQVEHPTTEMVSGVNI 377
DB 542 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPTTEMVSGVNI 600
QY 378 PAAQLQVANGIPLYISIRDIRTLGYMDPRGNEVIDDFDSSPESFKT-QRXPQOQHVVACR 436
DB 601 PAAQLQIANGVPLHRLKDIRLLYGSPWG-----VTFISFETPSNPLLARGHVIAAR 652
QY 437 ITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSFQGHIFAYGADRSE 496
DB 653 ITSENPDEGFKPSSGTVQELNFRSSKQWGYFVAATGGLHGFADSFQGHCFSGWENRKE 712
QY 497 ARKQWVLSKLSIRGDFRTTVEYLIKLETDAFESNKITTTGWLGLIOQLTAERPPAD 556
DB 713 AISNMVVALKLSIRGDFRTTVEYLIINLETESFQNNDDITGWLGLYIAEKV-QEKPDIM 771
QY 557 LAV 559
DB 772 LGV 774

RESULT 32
ADN03634
ID ADN03634 standard; protein; 2206 AA.
AC ADN03634;
DT 01-JUL-2004 (first entry)
XX Antipsoriatic protein sequence #14.
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
OS Homo sapiens.
XX W02004028479-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030907.
XX 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;
PI Wu TD;
XX WPI; 2004-305105/28.
DR N-PSDB; ADN03633.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 28; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX Sequence 2206 AA;
SQ

Query Match 58.4%; Score 1697.5; DB 8; Length 2206;
 Best Local Similarity 63.7%; Pred. No. 3.4e-149;
 Matches 324; Conservative 74; Mismatches 98; Indels 13; Gaps 4;

QY 54 IRSIRKWAYETFGDERAIEFTVMATPEDLKNADYIRMDQYVEVPGSGNNNNYANVDLI 113
 DB 1 MRSIRKWSYEMFRNERAIRFVVMVTPEDLKANAAYIKMADHYVPVPGPNNNYANVELI 60
 QY 114 VDVAERAGYHAWAGHCHASENRPLPESLAASHKIIIFGPPGSAWRSIGDKISSTIVAQ 173
 DB 61 LQIAKPIPVQAVWAGHCHASENPKLPPELL--KNGIAFMGPPSQAMWALGDKLIASSIVAQ 118
 QY 174 HADVPQWPSGTGIGKETTMSD---OGFLTVSDDDVYQACIHTAEGLAEKIGYPMWK 230
 DB 119 TAGIPTLPWSSGLRVDWQENDFSKILNVQELYEKGYVKVDDGLQAAEEVGYPMWK 178
 QY 231 ASEGGGKGIRKCTNGEEFKQLYNVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAI 290
 DB 179 ASEGGGKGIRKVNADDPNLFRQVAEVPGSPVFVRLAKQSRHLEVQLLADQYGNAI 238
 QY 291 SIFGRDCSVQRHOKIIIEAPVTIAPEDARESEKAARLAKLVGVYSGTVEWLYSPES 350
 DB 239 SLFGRDCSVQRHOKIIIEAPATIATPAVFEHMEQCAVKLAKMVGYSAGTVEYLYS-QD 297
 QY 351 GEFAPLELNPRLQVEHPTTEMUSGVNIPAAQLOVANGIPLYSIRDIRTYLGMDPRGNEVI 410
 DB 298 GSYFLELNPRLQVEHPTTEMADVNLPAQLOIANGIPLYIKDIRMYGVSPMGDSPI 357
 QY 411 DFDSPSPFKTQKQPQOHVVACRITAENPDPTGFKPGMGALTELNFRSSTSTWGYSFV 470
 DB 358 DFDSDA-----HYPCPRGHVIAARITSENDEGFKPSSGTVOELNFRSNKWNWGYFSV 410
 QY 471 GTSGLHLEVADQFGHIFAYGADRSEARKOMVISKELSIKELSIKELSIKELSIKELSIKEL 530
 DB 411 AAAGGLHEIADQFGHCFSGENREBAISNMVVALKELSIKELSIKELSIKELSIKELSIKEL 470
 QY 531 ESNKITTGWLDGLIQDLTAERPPADLAV 559
 DB 471 QMNRIDTGWLDRLIAEKVQARPDMLGV 499

RESULT 34
 ADQ90746
 ID ADQ90746 standard; protein; 2483 AA.
 XX AC ADQ90746;
 XX DT 21-OCT-2004 (first entry)
 XX DE Human acetyl-coenzyme A carboxylase - ACC2.
 XX KW human; carboxyltransferase domain; CT domain;
 KW acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase;
 KW metabolic syndrome; diabetes; obesity; cardiovascular disease;
 KW atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;
 KW hypertension; hyperuricaemia; renal dysfunction;
 KW crystallisable composition; enzyme; ACC2.
 XX OS Homo sapiens.
 XX PN WO2004063715-A2.
 XX PD 29-JUL-2004.
 XX PF 09-JAN-2004; 2004WO-US000585.
 XX PR 10-JAN-2003; 2003US-0439383P.
 PR 31-MAR-2003; 2003US-0459464P.
 PR 31-JUL-2003; 2003US-0491640P.
 PR 27-OCT-2003; 2003US-0514636P.
 PR 09-JAN-2004; 2004US-00514636.

(UYCO) UNIV COLUMBIA NEW YORK.
 Tong L, Zhang H, Yang Z;
 WPI; 2004-571486/55.
 New crystallisable composition comprising a carboxyltransferase domain of
 acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, obesity,
 cardiovascular disease, atherosclerosis, or cancer.
 Example 4; SEQ ID NO 9; 195pp; English.
 The invention comprises a crystallisable composition containing a
 carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA)
 carboxylase. The composition of the invention is useful for treating:
 metabolic syndrome, diabetes, obesity, cardiovascular disease,
 atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia,
 hypertension, hyperuricaemia and renal dysfunction. The present amino
 acid sequence represents a human acetyl-CoA carboxylase of the invention.

Query Match 57.4%; Score 1669.5; DB 8; Length 2483;
 Best Local Similarity 60.8%; Pred. No. 1.8e-146;
 Matches 330; Conservative 79; Mismatches 117; Indels 17; Gaps 8;

QY 22 ASPVADFIKOGGSHVITKVLICNNGIAAIVKXIRKWAYETFGDERAIEFTVMATPED 81
 DB 244 ASP-AEFTVTRPGDRIEKLVIANNGIAAIVKXIRKWAYETFGDERAIEFTVMATPED 302
 QY 82 LKNVADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGYHAWAGHCHASENRPLPES 141
 DB 303 LKANAYIKMADHYVPVPGPNNNYANVELIVDAERAGYHAWAGHCHASENRPLPES 362
 QY 142 LAASKHIIIFGPPG-SAMRSIGDKISSTIVAQHADVPQWPSGTGIGKETTMSD---QC- 196
 DB 363 LC--KNGVAFGLPRLRPMVGLGDKIATVVAQTLOVPTLPRSGSALTVEWTDLQOK 420
 QY 197 FLTSSDDVYQACIHTAEGLAEKIGYPMVMIKASEGGGKGIRKCTNGEEFKOLYNV 256
 DB 421 RISVPEDVYKGVKVDDEGLEAAERIGFPLMIKASEGGGKGIRKCTNGEEFKOLYNV 480
 QY 257 LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAIIFGDCSVQRHOKIIEAPVTIAP 316
 DB 481 QSEIPGSPFIFLMKLAQHARHLEVQLLADQYGNVSLFGDCSVQRHOKIIEAPVTIAP 540
 QY 317 EDARESEKAARLAKLVGVYSGTVEWLYSPESGEPAFLNPRLOVEHPTTEMVSGVN 376
 DB 541 LAIEFMEQCAIRLAKTVGVYSGTVEYLYS-QDGSFHFLELNPRLQVEHPTTEMADV 599
 QY 377 IPAAQLQVAMGIPLYSIRDIRTYLGMDPGRGNEVIDFDSPSPFKTQKQPQOHVVACR 436
 DB 600 LPAAQLQIAMGAPLHRLKDIRLLYGESWGDSPISFENSA-----HLPCPRGHVIA 652
 QY 437 ITAENPDPTGFKPGMGALTELNFRSSTSTWGYSFVGTSGALHLEYADSQGHIFAYGADRSE 496
 DB 653 ITSENPDGFKPSSGTVOELNFRSSTSTWGYSFVGTSGALHLEYADSQGHIFAYGADRSE 712
 QY 497 ARKOMVISKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKEL 556
 DB 713 AISNMVVALKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKELSIKEL 771
 QY 557 LAV 559
 DB 772 LGV 774

RESULT 34
 ADQ39507
 ID ADQ39507 standard; protein; 2483 AA.
 XX AC ADQ39507;
 XX

DT	18-NOV-2004	(first entry)	
XX	Human myocardial infarction-associated gene derived protein, SEQ ID 1170.		
DE	Myocardial infarction; detection; single nucleotide polymorphism; SNP;		
XX	cardiant; gene therapy; human.		
KW	Homo sapiens.		
XX	WO2004058052-A2.		
OS	15-JUL-2004.		
XX	22-DEC-2003; 2003WO-US040978.		
PN	20-DEC-2002; 2002US-0434778P.		
XX	10-MAR-2003; 2003US-0453135P.		
PR	30-APR-2003; 2003US-0466412P.		
XX	23-SEP-2003; 2003US-0504955P.		
XX	(APPL-) APPLERA CORP.		
PA	Cargill M, Devlin JJ, Takoubova O;		
XX	WPI; 2004-533949/51.		
PI	N-PSDB; ADQ38679.		
XX	Identifying an individual who has an altered risk for developing		
CC	myocardial infarction by detecting a single nucleotide polymorphism in		
CC	the individual's nucleic acids.		
PT	Claim 10; SEQ ID NO 1170; 145pp; English.		
XX	The invention relates to a novel method for identifying an individual who		
CC	has an altered risk for developing myocardial infarction. The method		
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of		
CC	the nucleotide sequences given in the specification in the individual's		
CC	nucleic acids, where the presence of the SNP is correlated with an		
CC	altered risk for myocardial infarction in the individual. The invention		
CC	further comprises: an isolated nucleic acid molecule comprising at least		
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in		
CC	the specification or its complement and encoding any one of the amino		
CC	acid sequences given in the specification; an isolated polypeptide		
CC	comprising an amino acid sequence given in the specification; an antibody		
CC	that specifically binds to the polypeptide or its antigen-binding		
CC	fragment; an amplified polynucleotide containing an SNP given in the		
CC	specification and which is between about 16 and 1000 nucleotides in		
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the		
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a		
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a		
CC	method for identifying an agent useful in treating or preventing		
CC	myocardial infarction. The novel detection method has cardiant activity.		
CC	The nucleic acids of the invention may be used in gene therapy. The		
CC	method is useful in identifying an individual who has an increased or		
CC	decreased risk for developing myocardial infarction and for preparing a		
CC	composition for treating or preventing myocardial infarction. This		
CC	sequence represents the protein of a human myocardial infarction-		
CC	associated gene containing one or more SNPs of the invention. Note: This		
CC	sequence was not shown in the specification. The sequence has come from		
CC	an electronic sequence listing downloaded from the WIPO website.		
XX	Sequence 2483 AA;		
XX	Query Match	57.4%; Score 1669.5; DB 8; Length 2483;	
XX	Best Local Similarity	60.8%; Pred. No. 1.9e-146;	
XX	Matches 330; Conservative	79; Mismatches 117; Indels 17; Gaps 8;	
QY	22 ASPVAFIRKQGHSHVITKVLICNGIAAIVKEIRSRKWAYETFGDBRAIEFTVMATPED 81		
DB	244 ASP-ABFVTRFGGDRVIEKVLIANNGIAAIVKCMRSIRRWAYEFRNERAIRFVRMTPTD 302		
QY	82 LKNYADYIRWADQYVEVPGSGNNNNYANVDLIVDVAERAGVHAVWAGWGHASNPRLPES 141		

Db	303	LKANAEYIKMADHYGAPGPGNNNNYANVELLIVDAKRIPLQAVWAGWGHALENPKLP 362
QY	142	LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPCMPWSGTGKITKMSD---QG- 196
Db	363	LC--KNGVAFLGPPRLRPMVGLGDKIASTVVAQTLQVPTLPRSGSALTVEWTEDDLLQOGK 420
QY	197	FLTVSDVVYQACIHTAEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEBEFKQLYNAY 256
Db	421	RISVPEDVYDKGVKXVDVDEGLEAABRIQFPLMIKASEGGGKGIRKCTNGEBEFKQLYNAY 480
QY	257	LGEVPGSPVFMKLAGQARHLEVLADQYGNALISIFGRDCSVQRRHOKIIEEAPVTIAP 316
Db	481	QSEIFGSPFLMKLAQAHLEVLADQYGNALISIFGRDCSVQRRHOKIIEEAPVTIAP 540
QY	317	EDARESMKAAVRLAKLVGYVSAGTVEMLYSPESGEFAFLELNPRLOVHEHPTTEMVSGVN 376
Db	541	LAIFFEMEQCAIRLAKTVGYVSAGTVVEVLYS-QDGSFHFLELNPRLOVHEHPTTEMVSGVN 599
QY	377	IPAAQLQVAMGIPLYSIRDITLYGMDPRGNEVIDFDSSPESFKTQPKPOQGHVACR 436
Db	600	LPAALQIANGAPLHRLKDIRLLYGESFWGDSPISENSA-----HLPCPRGHVIATR 652
QY	437	ITAENPDTGFKPGMGALTELNFRSSTWTGVSFVSGTSGALHEYADSQFGHIFAYADRSE 496
Db	653	ITSENPDGFKPSSGTVQELNFRSSKNVWGYFTVAATGGLHFEALSQFGHCFSGWGNRKE 712
QY	497	ARKQWISLSELSIRGDFRTTVEYLIILKLETDAPESNKITTWGLDGLIODRLTAERPPAD 556
Db	713	AISNMVVALKELSGDFRTTVEYLIILKLETDAPESNKITTWGLDGLIODRLTAERPPAD 771
QY	557	LAV 559
Db	772	LGV 774
RESULT 35		
AEA33628		
ID	AEA33628	standard; protein; 2483 AA.
AC	AEA33628;	
DT	28-JUL-2005	(first entry)
XX	Human ACC2 protein - SEQ ID 4.	
XX	obesity; diabetes; atherosclerosis; heart disease; ACC2.	
OS	Homo sapiens.	
XX	WO2005047525-A1.	
XX	26-MAY-2005.	
XX	15-NOV-2004; 2004WO-AU001572.	
XX	14-NOV-2003; 2003AU-00906285.	
PR	14-NOV-2003; 2003AU-00906286.	
XX	(GARV-) GARVAN INST MEDICAL RES.	
XX	James D, Cooney GJ, Molero-Navajas JC;	
XX	WPI; 2005-386363/39.	
DR	Identifying a modulator of whole body insulin sensitivity of an animal by	
PT	determining the AMP-dependent protein kinase or acetyl CoA carboxylase	
PT	activity or free fatty acid level or oxidation in the animal administered	
PT	with a compound.	
XX	Disclosure; SEQ ID NO 4; 296pp; English.	
XX	The invention comprises a method of identifying a compound that enhances	
CC	or reduces whole body insulin sensitivity of an animal. The method	

involves administering a compound to a non-human animal, isolated tissue or cell having reduced expression of functional multi-adaptor protein Cbl, and determining the activity of acetyl CoA carboxylase (ACC) and/or amount of phosphorylated ACC enzyme in the animal, tissue or cell. The method is useful for identifying a compound that enhances or reduces whole body insulin sensitivity of an animal, and for preparing a composition for the treatment of obesity, diabetes, atherosclerosis and heart disease. The present amino acid sequence represents a human ACC2 protein.

Sequence 2483 AA:

Query Match 57.4%; Score 1669.5; DB 9; Length 2483;
Best Local Similarity 60.8%; Pred. No. 1.8e-146;
Matches 330: Conservative 79; Mismatches 117. Indels 17.

QY	22	ASPVADIFIRKQGHSHSVITKVLCNNGIAAIVKEIRSIRKWAYETFGDGERAEFTVMATPED	81
Db	244	ASP-ABEFVTRFGGDRVIEKVLJIANNGIAAVCMRSIRRAWEMFPRNERARFRVRWVTTPED	302
QY	82	LKNVADYIRWADOYEVEPCGSNNNNYANVDLIVDVAERAGVHAWAGWGCHASHENPLPES	141
Db	303	LKANAEYIKWAHDYGPAEGPPGNPNNYANVELIVDIAKRIPLQAVWAGWHALENPKLPSEL	362
QY	142	LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPCMPWSGTGKETMMSD---	QG- 196
Db	363	LC--KNGVAFGLPPRLRPVWGDLGXIASTVVAQTLOVPTLPRSGSALTVEWTEDDLOQQK	420
QY	197	FUTVSDDVVQAACHTAEGLKAEPKIGYPVMIKASEGGGGKGIRKTNGEEFKQLYNVA	256
Db	421	RISVPEDVYDKGVKDVEDGLEAAERIGFPLMIKASEGGGGKGIRETSAEDFPILFRQV	480
QY	257	LCEVPGSPVFMVKLAGOARHLEVOALLADOYGNALSI FGRDCSVQRHQKIIEBAPVTIAP	316
Db	481	QSEIPGSPFIPLMKLAQHARHLEVOALLADOYGNVSLFGRDCSIQRHQKIVEEAPTATIAP	540
QY	317	EDARSEMKEAAVRLAKLVGYYSAGTVELWLYSPGESGEFAFLBNPLRQLOVEHPPTTEMVSGVN	376
Db	541	LAIPEMEQCAIRLAKTVGYYSAGTVELYLS-QDGSFHFLBNPLRQLOVEHPCTEMIADVN	599
QY	377	IIPAOLQVAMGIPLYISIBDIRTLXGMDPRGNEVIDDFSSPFKTKORQPQOGHYVACR	436
Db	600	LPAAOLOIAMGAPLRHLRKDIRLLYESPWGSDSPISENSA-----HLPCPRGHVIATR	652
QY	437	ITAEINPDGTFKPCMCALETALNFRSTSTGWYFSVGTSGALHEVADSOPGHIIFAYGADRSE	496
Db	653	ITSENPDGDFKPSSGTVQELNFRSSKNWGYFTVAATGTLHEFAISQFGHCFSWGENRKE	712
QY	497	ARKQNVISLKELSIRGDFRTTVEYLIIKLETDAPESNKITTGMLDGLIODRLTAERRPPAD	556
Db	713	ALSNMVVALKELSRGDFRTTVEYLINLLETESPQNYYIDTGMDYLIAEKV-QKKPNIM	771
QY	557	LAV 559	
Db	772	LGV 774	

RESULT 36

ADJ47652
ID ADJ47652 standard; protein; 555 AA.

AA
AC

DT 06-MAY-2004 (first entry)

DE P. infestans ACCase BC domain SEQ ID NO:4.

ACCase; Acetyl CoA carboxylase; carboxy transferase domain;
biotin carboxylase domain; BC domain; fungicide.

Phytophthora infestans.

XX
PN WO2004013159-A2.

PN WO2004013159-A2. 317 PTQEVWEKMMRAATRLAQOEYEVYNAGTVLEYFSELPEDNGNSFFLELNPRLQVEHPVTE 376 Db

XX PD XX PF XX PR XX PA XX PI XX DR XX FT PT PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC

Sequence 555 AA:

Query Match 55.2%; Score 1604; DB 8; Length 555;
Best Local Similarity 58.2%; Pred. No. 2.2e-141;
Matches 309; Conservative 81; Mismatches 123; Indels 1

QY	15	NPLETAPASVPADFIRKQGGHSHVTTKYLICNGIGAAVKEIRSIRKWAYETFGDERAIEFT	74
Db	23	NPLNYA---SMEEYVRLQKGRPITSVLIIANNGISAVKAIIRSRSYEMFADEHVVTfV	79
QY	75	VMAITPEDIKNADYIRWADQYVEVPGSGNNNNVANVDLIUDVAERAGVHVAWAGWGHASe	134
Db	80	VMAITPEDIKANAEYIRWAEHVVEVPGSGNNNNHNTANVSLIETIERENFNVDVAWAGWGHASe	139
QY	135	NPLRPESLAAASKHKIIFIGPPGSAMRSLGDKISTIVAOHADYPCPMSWSTGIGIKETMMSD	194
Db	140	NPLLPDTLUQATERKIVIFIGPPKPMRALGDKISTIIAOSAKVPTIAWNGDGVDEYKEH	199
QY	195	QGLFTVSDVVQQACIHTABEGLEKAEKIGYPVMIKASGGGGKGIKCTNGBEPKQLYN	254
Db	200	DG---IPDEIYNAMLRDGQHCLDECKRIGFPVMIKASGGGGKGIKMWHERSVOVLSAME	256
QY	255	AVLGEVPGSPVFMKLGAQARHLEVQLLADQYNAISIFGRDCSVORRHQKIIERAPVTI	314
Db	257	AVRGEIPGSPFVFMKLAPKSRHLEVQLLADTYGNAIALSGRDCSVORRHQKIVEEGPVLA	316
QY	315	APEDARESMEKAAVRLAKLVGYVSAGTVEWLYS--PE--SGSFAFLELNPRLQVHEPPTTE	370
Db	317	PTQEWKEMKMAAFTLQAQVEYVYNAAGTVYLFSELPEDNGNSFFFLFELNPRLQVHEPPTTE	376

QY 371 MVSGWNPAAQLQVAMGIPLYSIRDTITLYGMDBPRGNEVIDFDFSPSPFKTKRQPOQ 430
DB 377 MITHVNLPAQLQVAMGIPLYSIRDTITLYGMDBPRGNEVIDFDFSPSPFKTKRQPOQ 428
QY 431 HVVACRITARNPDTGFKPGMGALTELNFIRSTSTWGYFSGALHEVADSOFGHIFAY 490
DB 429 HVVACRITARNPDTGFKPGMGALTELNFIRSTSTWGYFSGALHEVADSOFGHIFAY 488
QY 491 GADSEARKQWISLKELSIRGDFRTTVEYLILKLETFDFAESNKITTTGMLD 541
DB 489 SPTRKARKQWISLKELSIRGDFRTTVEYLILKLETFDFAESNKITTTGMLD 539
RESULT 37
ADQ39504
ID ADQ39504 standard; protein; 1096 AA.
XX
AC ADQ39504;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1167.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 20-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
XX
DR WPI; 2004-533949/51.
DR N-PSDB; ADQ38676.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1167; 145pp; English.
XX
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1096 AA;
Query Match 54.7%; Score 1591.5; DB 8; Length 1096;
Best Local Similarity 58.1%; Pred. No. 1e-139;
Matches 315; Conservative 65; Mismatches 93; Indels 69; Gaps 6;
QY 22 ASPVADFKKQGHSHVITKVLICNNGIAAIVKIRKWAYETFGDERAIEFTVATPED 81
DB 245 ASP-AEFTVTRFGGDRVIEKVLIANNGIAAIVKIRKWAYETFGDERAIEFTVATPED 303
QY 82 LKVNADYIRMDADYVEVPGSGNNNNYANVLLVDVAERAGHAVAGWGHASENPRLPES 141
DB 304 LKANAAYIKMADHYVPVPGSGNNNNYANVLLVDIAKRIPVQAVWAGWGHASENPKLP 363
QY 142 LAASKHKHIFIGPPGSAVRSLGDKISSTIVAGADVPCWPSGSGTIGKTMMSD---QG-F 197
DB 364 LC--KNGVAFLLGPPSEAMWALGDKIASTVVAQTLQVPTLPWSSGGLTVEWTEDDLQOGKR 421
QY 198 LTVSDDVYQACIHTABEGLEKAEKIGYPMVKASEGGGKGIKCTNGEEFKOLYNVL 257
DB 422 ISVPEDVYDKGCVKDVDEGLEAERIGFPLMIKASEGGGKGIKCAESAEDEPILFRVQ 481
QY 258 GEVPGSPVFMKLAGOARHLEVOLLADOVGNASISIFGRDCSVORRHOKIIEBAPVTIPE 317
DB 482 SEIPSGPIFLMKLAQARHLEVOLLADOVGNASISIFGRDCSVORRHOKIIEBAPVTIPE 541
QY 318 DARESMKAAVRLAKLVGYVSAGTYEWLYSPESGEGFAFLNLPRLQVEHPTTMSVGVNI 377
DB 542 ALIFEFMEQCAIRLAKTVGVVSAGTYEVLVS-QDGSFHFLELNPRLQVEHPTTMSVGVNI 600
QY 378 PAAQLQVAMGIPLYSIRDTITLYGMDBPRGNEVIDFDFSPSPFKTKRQPOQGHVACRI 437
DB 601 PAAQLQ----- 606
QY 438 TAENPDTGFKPGMGALTELNFIRSTSTWGYFSGALHEVADSOFGHIFAYGADRSEA 497
DB 607 -----GFKSSGTVQELNFRSSKNVWGYFSAVATGGLHEPADSOFGHIFAYGADRSEA 659
QY 498 RKQWISLKELSIRGDFRTTVEYLILKLETFDFAESNKITTTGMLDGLIQRLTAERPPADL 557
DB 660 ISNMVVALKELSIKRGDFRTTVEYLILKLETFDFAESNKITTTGMLDGLIQRLTAERPPADL 719
QY 558 AV 559
DB 720 GV 721
RESULT 38
AAU32848
ID AAU32848 standard; protein; 2486 AA.
XX
AC AAU32848;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #3339.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX

Db 280 PPSSLVITPEENMYRQACVYTTBEAASCOVGVYPAMIKASWGGGKGIRKVVHDDDEVRA 339
 QY 252 LYNALGEVPGSPVFMKLAGARHLEVLQADQYGNALISIFORDCSVORRHOKIIEEAP 311
 Db 340 LFKQVQGEVPGSPFIFMKVASQSRHLEVLQCDQYGNVSALHSRDCSVORRHOKIIEEGP 399
 QY 312 VTIAPEDARESMEKAAVRLAKLVGYVSAGTVLEWLYSPESGEPAFLNPRLOVEHPTTEM 371
 Db 400 ITVAPRDTVKLQQAARRLAKSNVYGAATVEFLYSMDTGDFLELNPRLQVEHPTVR 459
 QY 372 VSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDDFSSPESFKTORKPOQGH 431
 Db 460 IADINLPAAQVAVGMGIPLWQIPEIRRFYIEQYDSWRITSLILASFPNFDKAEVRFKGH 519
 QY 432 VVACRTAENPDPTGPKPGMGALTELNFRSSTSTWGFVSQTSALHEYADSQGHIPAYG 491
 Db 520 CVAVRVTSEDDPDGFKPTSGVQQLSFKSNPNWGYFVSQSGGIEHFSQSGHVFAG 579
 QY 492 ADSEARKOMVISLKELSIRGDPRTTVEYLILKLETDAPESNKITTTGWLDDGLIQDLTAE 551
 Db 580 ESPAMAIANVLAKKEIQIRGEVRTNVDYITDILHAFDYRENKIHTGWLDSRIAMRVRAE 639
 QY 552 RPPADLAV 559
 Db 640 RPPWYLSV 647

RESULT 40

ID ABB91251
 AC ABB91251 standard; protein; 2359 AA.

AC ABB91251;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 462.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP009892.

PR 28-AUG-2001; 2001WO-EP009892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
 comprising aligning and comparing nucleic acid or amino acid sequences
 from plant with nucleic acid or amino acid sequences from non-plant
 organisms.

PS Claim 5; SEQ ID NO 462; 26lpp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 for herbicidally active compounds, comprising aligning and comparing
 nucleic acid or amino acid sequences from plant with nucleic acid or
 amino acid sequences from non-plant organisms using suitable search
 parameters, where plant sequences having an E-value greater by a factor
 of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 identifying modulators. The identified modulators are useful as
 herbicides

SQ Sequence 2359 AA;

Query Match 54.4%; Score 1581.5; DB 5; Length 2359;
 Best Local Similarity 53.3%; Pred. No. 3.3e-138;
 Matches 305; Conservative 95; Mismatches 137; Indels 35; Gaps 8;

QY 12 IGGNPLETAPASPVA---DFIRKQGGHSHVITKVLICNNIGAAVKIERSIRKWAYETFGDE 68
 Db 110 VNGYHSDVVGENVAEVNEPCFKGLGKPIHSILVATNGMAAVKFIKSVRTWAYETFGSE 169
 QY 69 RAIEFTVMATPEDLKVNADYIRMDQYVEVPGSGNNNNYANVDLIVDAERAGVHAWAG 128
 Db 170 KAVKLIVAMATPEDMRINAEHRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVDVWEG 229
 QY 129 WGHASENPRLESIAASHK-IIFIGPPGSAMRSIGDKISSTIVAAHADVPCMPMSGTGI 187
 Db 230 WGHASENPELPDAL---KEKGLIIFGPPADSMIAUGDKISLSLIAQAADVPTLPMSGSIV 286
 QY 188 KETWMSDQGLTVSDVYQQACIHTAEGLKAEKIGYPVMIKASEGGGKGIRKCTNGE 247
 Db 287 K--IPGRLVTVPEIYKACVYITEAIAISCOVVGYPAMIKASWGGGKGIRKVNDD 344
 QY 248 EFKQLYNALVGEVPGSPVFMKLAGARHLEVLQADQYGNALISIFGRDCSVORRHOKII 307
 Db 345 EVRALFKVQGEVPGSPFIFMKVASQSRHLEVLQCDQYGNVAALHSRDCSVORRHOKII 404
 QY 308 BEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVLEWLYSPESGEPAFLNPRLOVEHP 367
 Db 405 EGPITVAPQETIKLEQAARRLAKSNVYGAATVEYLISMDTGDFLELNPRLQVEHP 464
 QY 368 TTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRG-----NEVI--DFDFSSPE 418
 Db 465 VTEWIAEYNLPAQVAVGMGIPLWQIPEIRRFYGMHGGGYSWRKTSVVASPFDPDEAE 524
 QY 419 SFKORKPOQGHVAVACRITAEINPDPTGPKPGMGALTELNFRSSTSTWGFVSQTSALHE 478
 Db 525 SLR-----PKGHCVAVRVTSEDDPDGFKPTSGEIQELSFKSKPNMWSYFSKSGGGIHE 578
 QY 479 YADSQF-----HIFAYGADRSEARKQWISLKELSIRGDPRTTVEYLILKLETT 527
 Db 579 FSDSQFGKLNKFGMLGQHVFAFGESRSVAIANMVLAKKEIQIRGINVDITNVDITDILHA 638
 QY 528 DAFESNKITTTGWLDDGLIQDLTAERPPADLAV 559
 Db 639 SDYRENKIHTGWLDSRIAMRVRAERPPWYLSV 670

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